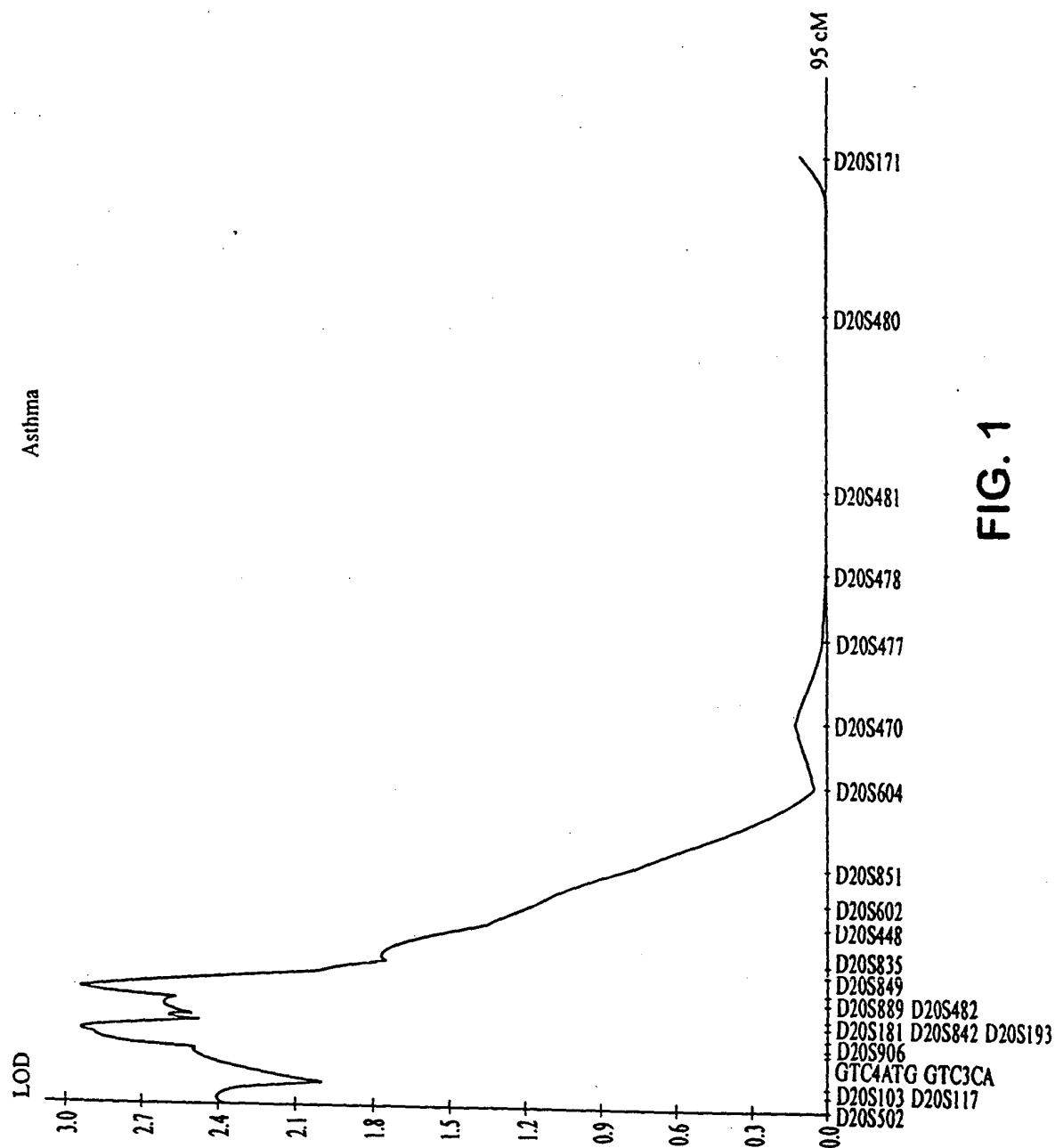


Asthma



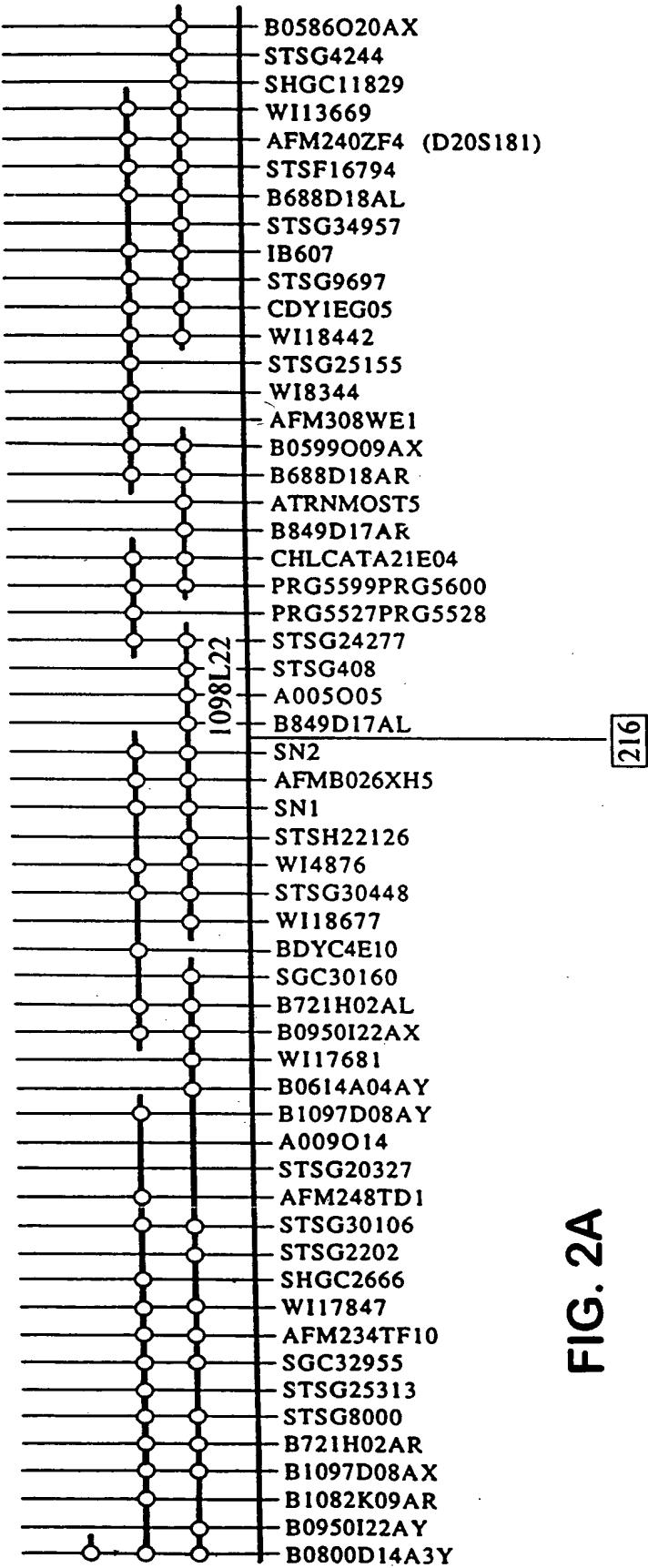


FIG. 2A

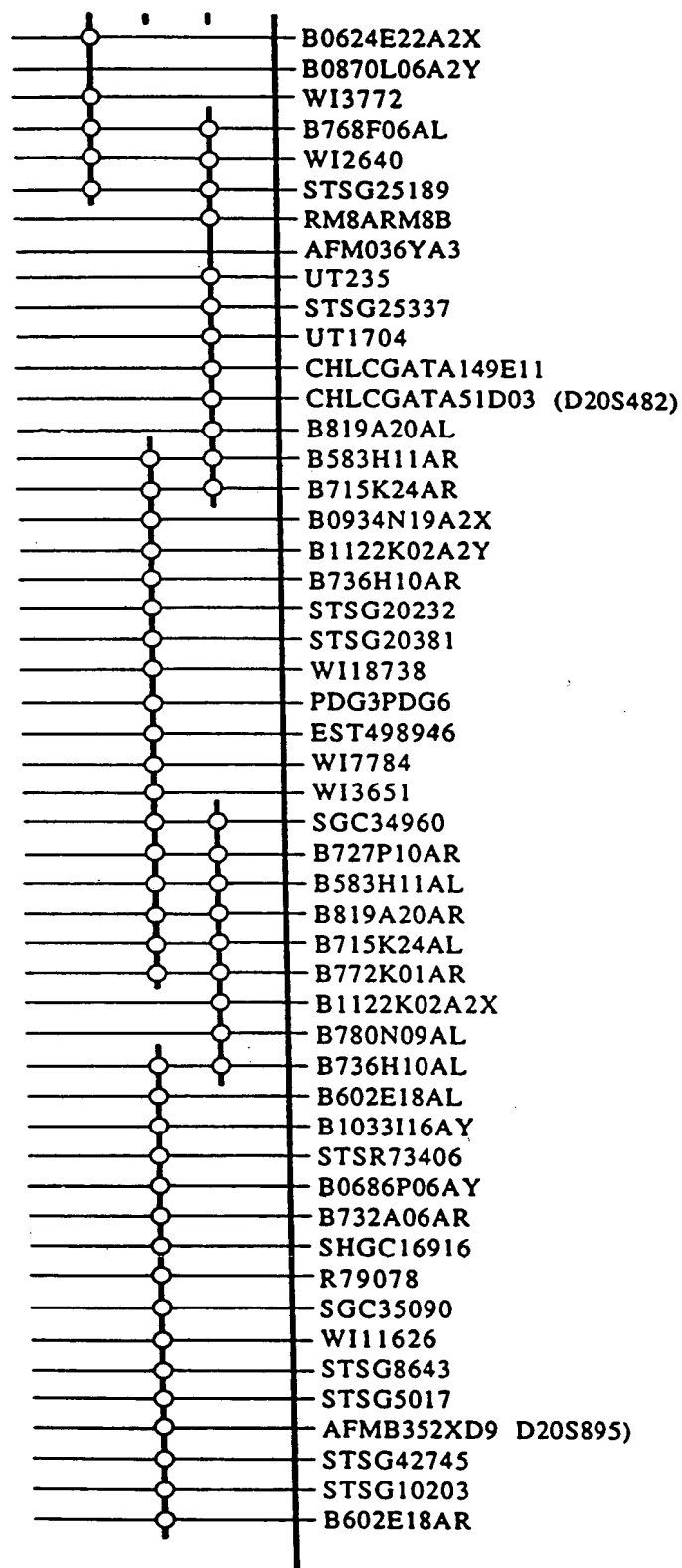


FIG. 2B

10 30 50
 ATGGGCTGGAGCCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTACTGCTG
 MetGlyTrpArgProArgArgAlaArgGlyThrProLeuLeuLeuLeuLeuLeuLeuLeu

70 90 110
 CTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGACATATCCCTGGGCAGCCAGTC
 LeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyHisIleProGlyGlnProVal

130 150 170
 ACCCCGCACTGGGTCCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTC
 ThrProHisTrpValLeuAspGlyGlnProTrpArgThrValSerLeuGluGluProVal

190 210 230
 TCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAG
 SerLysProAspMetGlyLeuValAlaLeuGluAlaGluGlyGlnGluLeuLeuLeuGlu

250 270 290
 CTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCCAGAT
 LeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIleGluThrHisTyrGlyProAsp

310 330 350
 GGGCAGCCAGTGGTGCTGGCCCCCAACCACACGGATCATTGCCACTACCAAGGGCGAGTA
 GlyGlnProValValLeuAlaProAsnHisThrAspHisCysHisTyrGlnGlyArgVal

370 390 410
 AGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCCTGATC
 ArgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyLeuIle

430 450 470
 ACCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGAC
 ThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAsp

490 510 530
 TTCTCAACCCACGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGC
 PheSerThrHisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrCysGly

550 570 590

FIG. 3A

CACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGAGCAGG
HisArgAspProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlnSerArg

610 630 650

GGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCAC
GlyArgArgGluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaAspHis

670 690 710

ACCCTGTTCTTGACTCGGCACCGAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTC
ThrLeuPheLeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluVal

730 750 770

GCCAACTACGTGGACCAGCTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCGGCCTG
AlaAsnTyrValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrGlyLeu

790 810 830

GAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGG
GluValTrpThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrLeuTrp

850 870 890

GCCTTCCTGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTG
AlaPheLeuGlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaGlnLeu

910 930 950

CTCACGGGCCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGC
LeuThrGlyArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyMetCys

970 990 1010

CGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCGCCGCA
ArgAlaGluSerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyAlaAla

1030 1050 1070

GCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGC
AlaThrMetAlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspGlyCys

1090 1110 1130

TGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCG
CysValGluAlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyHisPro

FIG. 3B

1150 1170 1190
TTTCCGCGCGTGTTCAGCGCCTGCAGCCGCCAGCTGCGCGCCTTCTTCCGCAAGGGG
PheProArgValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgLysGly

1210 1230 1250
GGCGGCGCTTGCCTCTCCAATGCCCCGGACCCCGGACTCCC GGTTGCCGCCGGCGCTCTGC
GlyGlyAlaCysLeuSerAsnAlaProAspProGlyLeuProValProProAlaLeuCys

1270 1290 1310
GGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGTGCCGC
GlyAsnGlyPheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluCysArg

1330 1350 1370
GACCTCTGCTGCTTTGCTCACAACCTGCTCGCTGCGCCCCGGGGGCCAGTGCGCCACGGG
AspLeuCysCysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaHisGly

1390 1410 1430
GACTGCTGCGTGCGCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGT
AspCysCysValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaMetGly

1450 1470 1490
GACTGTGACCTCCCTGAGTTTTGCACGGGCACCTCCTCCCACTGTCCCCCAGACGTTTAC
AspCysAspLeuProGluPheCysThrGlyThrSerSerHisCysProProAspValTyr

1510 1530 1550
CTACTGGACGGCTCACCCCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCC
LeuLeuAspGlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaCysPro

1570 1590 1610
ACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCCCTGATGGCCAGGAAGTGACTTGTCGG
ThrLeuGluGlnGlnCysGlnGlnLeuTrpGlyProAspGlyGlnGluValThrCysArg

1630 1650 1670
GGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAGCCA
GlyAlaLeuAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGlyLeuValGluPro

1690 1710 1730

FIG. 3C

GGCACCCAGTGTGGACCTAGAATGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTC
GlyThrGlnCysGlyProArgMetValCysGlnSerArgArgCysArgLysAsnAlaPhe

1750

1770

1790

CAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTTGCAATAGCAACCAT
GlnGluLeuGlnArgCysLeuThrAlaCysHisSerHisGlyValCysAsnSerAsnHis

1810

1830

1850

AACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGC
AsnCysHisCysAlaProGlyTrpAlaProProPheCysAspLysProGlyPheGlyGly

1870

1890

1910

AGCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCCTGCTGGCCATGCTC
SerMetAspSerGlyProValGlnAlaGluAsnHisAspThrPheLeuLeuAlaMetLeu

1930

1950

1970

CTCAGCCTCCTGCTGCCTCTGCTCCCAGGGCCGGCCTGGCCTGGTGTGCTACCGACTC
LeuSerThrLeuLeuProLeuLeuProGlyAlaGlyLeuAlaTrpCysCysTyrArgLeu

1990

2010

2030

CCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGGC
ProGlyAlaHisLeuGlnArgCysSerTrpGlyCysArgArgAspProAlaCysSerGly

2050

2070

2090

CCCAAAGATGGCCACACAGGGACCACCCCTGGGCGGCGTTCACCCCATGGAGTTGGGC
ProLysAspGlyProHisArgAspHisProLeuGlyGlyValHisProMetGluLeuGly

2110

2130

2150

CCCACAGCCACTGGACAGCCCTGGCCCTGGACCCTGAGAACTCTCATGAGCCAGCAGC
ProThrAlaThrGlyGlnProTrpProLeuAspProGluAsnSerHisGluProSerSer

2170

2190

2210

CACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGCAGATCAAGTCCAGATG
HisProGluLysProLeuProAlaValSerProAspProGlnAlaAspGlnValGlnMet

2230

2250

2270

CCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGG
ProArgSerCysLeuTrpEnd

FIG. 3D

2290 2310 2330
CCACTGACAGCCACTCCAGGAAGTTGAACTGCAGGGGCAGAGCCAGTGAATCACCGGACC

2350 2370 2390
TCCAGCACCTGCAGGCAGCTTGGAAGTTCTTCCCCGAGTGGAGCTTCGACCCACCCACT

2410 2430 2450
CCAGGAACCCAGAGCCACATTAGAAAGTTCCTGAGGGCTGGAGAACACTGCTGGGCACACT

2470 2490 2510
CTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCCTGACCTCCCTC

2530 2550 2570
ACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCAAAGGGCTCTGTCCTGGGAGTCTGGTG

2590 2610 2630
TGTCTCTACATGCAATTTCCACGGACCCAGCTCTGTGGAGGGCATGACTGCTGGCCAGA

2650 2670 2690
AGCTAGTGGTCCTGGGGCCCTATGGTTCGACTGAGTCCACACTCCCCTGCAGCCTGGCTG

2710 2730 2750
GCCTCTGCAAACAAACATAATTTTGGGGACCTTCCTTCCTGTTTCTTCCCACCCTGTCTT

2770 2790 2810
CTCCCCCTAGGTGGTTCCTGAGCCCCCACCCTCAATCCCAGTGCTACACCTGAGGTTCTGG

2830 2850 2870
AGCTCAGAATCTGACAGCCTCTCCCCATTCTGTGTGTGTCTCGGGGGGACAGAGGGAACCA

2890 2910 2930
TTTAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAGACATGTTGGCTATAGGCGTGGTG

FIG. 3E

2950	2970	2990
GCTCATGCCTATAATCCCAGCACTTTGGGAAGCCGGGGTAGGAGGATCACCAGAGGCCAG		
3010	3030	3050
GAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTAAAA		
3070	3090	3110
TTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAG		
3130	3150	3170
GATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGGCACCCTGCACTCCAGC		
3190	3210	3230
CTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAAGACATATTAAAAAA		
3250	3270	
AAAAAAAAAAAAAAAAAAAAAAAAAAAA		

FIG. 3F

10 30 50
 ATGGGCTGGAGGCCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTACTGCTG
 MetGlyTrpArgProArgArgAlaArgGlyThrProLeuLeuLeuLeuLeuLeuLeuLeu

70 90 110
 CTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGACATATCCCTGGGCAGCCAGTC
 LeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyHisIleProGlyGlnProVal

130 150 170
 ACCCGCACTGGGTCCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTC
 ThrProHisTrpValLeuAspGlyGlnProTrpArgThrValSerLeuGluGluProVal

190 210 230
 TCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAG
 SerLysProAspMetGlyLeuValAlaLeuGluAlaGluGlyGlnGluLeuLeuGlu

250 270 290
 CTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCCAGAT
 LeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIleGluThrHisTyrGlyProAsp

310 330 350
 GGGCAGCCAGTGGTGGTGGCCCCCAACCACACGGATCATTGCCACTACCAAGGGCGAGTA
 GlyGlnProValValLeuAlaProAsnHisThrAspHisCysHisTyrGlnGlyArgVal

370 390 410
 AGGGGCTTCCCCGACTCCTGGGTAGTCTCTGCACCTGCTCTGGGATGAGTGGCCTGATC
 ArgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyLeuIle

430 450 470
 ACCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGAC
 ThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAsp

490 510 530
 TTCTCAACCCACGAGATCTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGC
 PheSerThrHisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrCysGly

550 570 590

FIG. 4A

CACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGAGCAGG
HisArgAspProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlnSerArg

610

630

650

GGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAACGTACATTGTGGCAGACCAC
GlyArgArgGluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaAspHis

670

690

710

ACCCTGTTCTTGACTCGGCACCGAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTC
ThrLeuPheLeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluVal

730

750

770

GCCAACTACGTGGACCAGCTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCGGCCTG
AlaAsnTyrValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrGlyLeu

790

810

830

GAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGG
GluValTrpThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrLeuTrp

850

870

890

GCCTTCCTGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTG
AlaPheLeuGlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaGlnLeu

910

930

950

CTCACGGGCCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGC
LeuThrGlyArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyMetCys

970

990

1010

CGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCGCCGCA
ArgAlaGluSerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyAlaAla

1030

1050

1070

GCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGC
AlaThrMetAlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspGlyCys

1090

1110

1130

TGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCG
CysValGluAlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyHisPro

FIG. 4B

1150	1170	1190
TTTCCGCGCGTGTTCAGCGCCTGCAGCCGCCAGCTGCGCGCCTTCTTCCGCAAGGGG		
PheProArgValPheSerAlaCysSerArgArgGlnLeuArg <u>Ala</u> PhePheArgLysGly		
1210	1230	1250
GGCGGCGCTTGCCTCTCCAATGCCCCGGACCCCGGACTCCCGGTGCCGCCGGCGCTCTGC		
GlyGlyAlaCysLeuSerAsnAlaProAspProGlyLeuProValProProAlaLeuCys		
1270	1290	1310
GGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGTGCCGC		
GlyAsnGlyPheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluCysArg		
1330	1350	1370
GACCTCTGCTGCTTTGCTCACAACCTGCTCGCTGCGCCCGGGGGCCAGTGCGCCACGGG		
AspLeuCysCysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaHisGly		
1390	1410	1430
GACTGCTGCGTGCGCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGT		
AspCysCysValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaMetGly		
1450	1470	1490
GACTGTGACCTCCCTGAGTTTTGCACGGGCACCTCCTCCCACTGTCCCCAGACGTTTAC		
AspCysAspLeuProGluPheCysThrGlyThrSerSerHisCysProProAspValTyr		
1510	1530	1550
CTACTGGACGGCTCACCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCC		
LeuLeuAspGlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaCysPro		
1570	1590	1610
ACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCCTGGCTCCCACCCAGCTCCCGAGGCC		
ThrLeuGluGlnGlnCysGlnGlnLeuTrpGlyProGlySerHisProAlaProGluAla		
1630	1650	1670
TGTTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGCGAG		
CysPheGlnValValAsnSerAlaGlyAspAlaHisGlyAsnCysGlyGlnAspSerGlu		
1690	1710	1730

FIG. 4C

GGCCACTTCCTGCCCTGTGCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGT
 GlyHisPheLeuProCysAlaGlyArgAspAlaLeuCysGlyLysLeuGlnCysGlnGly

1750 1770 1790
 GGAAAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGAAGCTCTACCGTTACCTAGAT
 GlyLysProSerLeuLeuAlaProHisMetValProValAspSerThrValHisLeuAsp

1810 1830 1850
 GGCCAGGAAGTGACTTGTCGGGGAGCCTTGGAAGTCCCAAGTGCCAGCTGGACCTGCTT
 GlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLeuAspLeuLeu

1870 1890 1910
 GGCCTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTTTGAATAGCAAC
 GlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCysAsnSerAsn

1930 1950 1970
 CATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGT
 HisAsnCysHisCysAlaProGlyTrpAlaProProPheCysAspLysProGlyPheGly

1990 2010 2030
 GGCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCCTGCTGGCCATG
 GlySerMetAspSerGlyProValGlnAlaGluAsnHisAspThrPheLeuLeuAlaMet

2050 2070 2090
 CTCCTCAGCGTCTGCTGCCTCTGCTCCAGGGGCGGCTGGCCTGGTGTGCTACCGA
 LeuLeuSerValLeuLeuProLeuLeuProGlyAlaGlyLeuAlaTrpCysCysTyrArg

2110 2130 2150
 CTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCACT
 LeuProGlyAlaHisLeuGlnArgCysSerTrpGlyCysArgArgAspProAlaCysSer

2170 2190 2210
 GGCCCCAAAGATGGCCACACAGGGACCACCCCTGGGCGGCGTTACCCCATGGAGTTG
 GlyProLysAspGlyProHisArgAspHisProLeuGlyGlyValHisProMetGluLeu

2230 2250 2270
 GGCCCCACAGCCACTGGACAGCCCTGGCCCTGGACCCTGAGAACTCTCATGAGCCCAGC
 GlyProThrAlaThrGlyGlnProTrpProLeuAspProGluAsnSerHisGluProSer

FIG. 4D

2290 2310 2330
AGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGCAGATCAAGTCCAG
SerHisProGluLysProLeuProAlaValSerProAspProGlnAlaAspGlnValGln

2350 2370 2390
ATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGG
MetProArgSerCysLeuTrpEnd

2410 2430 2450
TGGCCACTGACAGCCACTCCAGGAAGTTGAACTGCAGGGGCAGAGCCAGTGAATCACCGG

2470 2490 2510
ACCTCCAGCACCTGCAGGCAGCTTGAAGTTTCTTCCCCGAGTGGAGCTTCGACCCACCC

2530 2550 2570
ACTCCAGGAACCCAGAGCCACATTAGAAGTTCCTGAGGGCTGGAGAACACTGCTGGGCAC

2590 2610 2630
ACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCCTGACCTCC

2650 2670 2690
CTCACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCCAAAAGGGCTCTGTCCTGGGAGTCTG

2710 2730 2750
GTGTGTCTCCTACATGCAATTTCCACGGACCCAGCTCTGTGGAGGGCATGACTGCTGGCC

2770 2790 2810
AGAAGCTAGTGGTCCTGGGGCCCTATGGTTCGACTGAGTCCACACTCCCCCTGCAGCCTGG

2830 2850 2870
CTGGCCTCTGCAAACAAACATAATTTTGGGGACCTTCCTTCCTGTTTCTTCCCACCCCTGT

2890 2910 2930
CTTCTCCCCTAGGTGGTTCCTGAGCCCCCACCCTCAATCCCAGTGCTACACCTGAGGTTT

FIG. 4E

2950 2970 2990
TGGAGCTCAGAATCTGACAGCCTCTCCCCATTCTGTGTGTGTCGGGGGGACAGAGGGAA

3010 3030 3050
CCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAGACATGTTGGCTATAGGCGTG

3070 3090 3110
GTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCCGGGGTAGGAGGATCACCAGAGGC

3130 3150 3170
CAGGAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTTA

3190 3210 3230
AAATTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAG

3250 3270 3290
GAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGGCACCACTGCACTCC

3310 3330 3350
AGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAAGACATATTAAAA

3370 3390
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 4F

10 30 50
ATGGGCTGGAGGCCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTACTGCTG
MetGlyTrpArgProArgArgAlaArgGlyThrProLeuLeuLeuLeuLeuLeuLeuLeu

70 90 110
CTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGTGAGGACGCGGGCGGGGTCCCC
LeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyGluAspAlaGlyGlyValPro

130 150 170
CTCACCTGTGCTCTGTCTTTACTCCAGGACATATCCCTGGGCAGCCAGTCACCCCGCAC
LeuThrLeuCysSerValPheThrProGlyHisIleProGlyGlnProValThrProHis

190 210 230
TGGGTCTTGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTCTCGAAGCCA
TrpValLeuAspGlyGlnProTrpArgThrValSerLeuGluGluProValSerLysPro

250 270 290
GACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAG
AspMetGlyLeuValAlaLeuGluAlaGluGlyGlnGluLeuLeuLeuGluLeuGluLys

310 330 350
AACCACAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCCAGATGGGCAGCCA
AsnHisArgLeuLeuAlaProGlyTyrIleGluThrHisTyrGlyProAspGlyGlnPro

370 390 410
GTGGTGCTGGCCCCCAACCACACGGATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTC
ValValLeuAlaProAsnHisThrAspHisCysHisTyrGlnGlyArgValArgGlyPhe

430 450 470
CCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCCTGATCACCTCAGC
ProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyLeuIleThrLeuSer

490 510 530
AGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACC
ArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAspPheSerThr

550 570 590

FIG. 5A

CACGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGAT
HisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrCysGlyHisArgAsp

610

630

650

CCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGAGCAGGGGCAGGCGA
ProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlnSerArgGlyArgArg

670

690

710

GAAGCGCGCAGGACCCGGAAGTACCTGGAACGTACATTGTGGCAGACCACACCCTGTTC
GluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaAspHisThrLeuPhe

730

750

770

TTGACTCGGCACCGAAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTCGCCAACTAC
LeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluValAlaAsnTyr

790

810

830

GTGGACCAGCTTCTCAGGACTCTGGACATTTCAGGTGGCGCTGACCGCCTGGAGGTGTGG
ValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrGlyLeuGluValTrp

850

870

890

ACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGGGCCTTCCTG
ThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrLeuTrpAlaPheLeu

910

930

950

CAGTGGCGCCGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGCTCACGGGC
GlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaGlnLeuLeuThrGly

970

990

1010

CGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGCCGCGCCGAG
ArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyMetCysArgAlaGlu

1030

1050

1070

AGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCGCCGCAGCCACCATG
SerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyAlaAlaAlaThrMet

1090

1110

1130

GCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGCTGCGTGGAG
AlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspGlyCysCysValGlu

FIG. 5B

1150 1170 1190
GCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCGTTTCCGCGC
AlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyHisProPheProArg

1210 1230 1250
GTGTTTCAGCGCCTGCAGCCGCCGAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCT
ValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgLysGlyGlyGlyAla

1270 1290 1310
TGCCTCTCCAATGCCCCGGACCCCGGACTCCCGGTGCCGCCGGCGCTCTGCGGGAACGGC
CysLeuSerAsnAlaProAspProGlyLeuProValProProAlaLeuCysGlyAsnGly

1330 1350 1370
TTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGTGCCGCGACCTCTGC
PheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluCysArgAspLeuCys

1390 1410 1430
TGCTTTGCTCACAACCTGCTCGCTGCGCCCCGGGGGCCAGTGCGCCACGGGGACTGCTGC
CysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaHisGlyAspCysCys

1450 1470 1490
GTGCGCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGAC
ValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaMetGlyAspCysAsp

1510 1530 1550
CTCCCTGAGTTTTGCACGGGCACCTCCTCCCACTGTCCCCAGACGTTTACCTACTGGAC
LeuProGluPheCysThrGlyThrSerSerHisCysProProAspValTyrLeuLeuAsp

1570 1590 1610
GGCTCACCCCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCACGCTGGAG
GlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaCysProThrLeuGlu

1630 1650 1670
CAGCAGTGCCAGCAGCTCTGGGGGCCTGGCTCCCACCCAGCTCCCGAGGCCTGTTTCCAG
GlnGlnCysGlnGlnLeuTrpGlyProGlySerHisProAlaProGluAlaCysPheGln

1690 1710 1730

FIG. 5C

GTGGTGA·A·C·T·C·T·G·C·G·G·G·A·G·A·T·G·C·T·C·A·T·G·G·A·A·A·C·T·G·C·G·G·C·C·A·G·G·A·C·A·G·C·G·A·G·G·G·C·C·A·C·T·T·C·
ValValAsnSerAlaGlyAspAlaHisGlyAsnCysGlyGlnAspSerGluGlyHisPhe

1750

1770

1790

C·T·G·C·C·C·T·G·T·G·C·A·G·G·G·A·G·G·G·A·T·G·C·C·C·T·G·T·G·T·G·G·G·A·A·G·C·T·G·C·A·G·T·G·C·C·A·G·G·G·T·G·G·A·A·G·C·C·C·
LeuProCysAlaGlyArgAspAlaLeuCysGlyLysLeuGlnCysGlnGlyGlyLysPro

1810

1830

1850

A·G·C·C·T·G·C·T·C·G·C·A·C·C·G·C·A·C·A·T·G·G·T·G·C·C·A·G·T·G·G·A·C·T·C·T·A·C·C·G·T·T·C·A·C·C·T·A·G·A·T·G·G·C·C·A·G·G·A·A·
SerLeuLeuAlaProHisMetValProValAspSerThrValHisLeuAspGlyGlnGlu

1870

1890

1910

G·T·G·A·C·T·T·G·T·C·G·G·G·A·G·C·C·T·T·G·G·C·A·C·T·C·C·C·C·A·G·T·G·C·C·C·A·G·C·T·G·G·A·C·C·T·G·C·T·T·G·G·C·C·T·G·G·G·C·
ValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGly

1930

1950

1970

C·T·G·G·T·A·G·A·G·C·C·A·G·G·C·A·C·C·C·A·G·T·G·T·G·G·A·C·C·T·A·G·A·A·T·G·G·T·G·T·G·C·C·A·G·A·G·C·A·G·G·C·G·C·T·G·C·A·G·G·
LeuValGluProGlyThrGlnCysGlyProArgMetValCysGlnSerArgArgCysArg

1990

2010

2030

A·A·G·A·A·T·G·C·C·T·T·C·C·A·G·G·A·G·C·T·T·C·A·G·C·G·C·T·G·C·C·T·G·A·C·T·G·C·C·T·G·C·C·A·C·A·G·C·C·A·C·G·G·G·G·T·T·T·G·C·
LysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCysHisSerHisGlyValCys

2050

2070

2090

A·A·T·A·G·C·A·A·C·C·A·T·A·A·C·T·G·C·C·A·C·T·G·T·G·C·T·C·C·A·G·G·C·T·G·G·G·C·T·C·C·A·C·C·T·T·C·T·G·T·G·A·C·A·A·G·C·C·A·
AsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaProProPheCysAspLysPro

2110

2130

2150

G·G·C·T·T·T·G·G·T·G·G·C·A·G·C·A·T·G·G·A·C·A·G·T·G·G·C·C·C·T·G·T·G·C·A·G·G·C·T·G·A·A·A·A·C·C·A·T·G·A·C·A·C·C·T·T·C·C·T·G·
GlyPheGlyGlySerMetAspSerGlyProValGlnAlaGluAsnHisAspThrPheLeu

2170

2190

2210

C·T·G·G·C·C·A·T·G·C·T·C·C·T·C·A·G·C·G·T·C·C·T·G·C·T·C·C·T·C·T·G·C·T·C·C·C·A·G·G·G·G·C·C·G·G·C·C·T·G·G·C·C·T·G·G·T·G·T·
LeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGlyAlaGlyLeuAlaTrpCys

2230

2250

2270

T·G·C·T·A·C·C·G·A·C·T·C·C·C·A·G·G·A·G·C·C·C·A·T·C·T·G·C·A·G·C·G·A·T·G·C·A·G·C·T·G·G·G·G·C·T·G·C·A·G·A·A·G·G·G·A·C·C·C·T·
CysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyCysArgArgAspPro

FIG. 5D

2290 2310 2330
GCGTGCAGTGGCCCCAAAGATGGCCCCACACAGGGACCACCCCTGGGCGGCGTTCACCCC
AlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuGlyGlyValHisPro

2350 2370 2390
ATGAGTTGGCCCCACAGCCACTGGACAGCCCTGGCCCCCTGGCCCCAGGGTCTCCTGCT
MetGluLeuGlyProThrAlaThrGlyGlnProTrpProLeuAlaProGlySerProAla

2410 2430 2450
GACCATATTCAACATTTACCCTCCACCATTCTCTCCAGACCCTGAGAACTCTCATGAG
AspHisIleHisAsnIleTyrProProProPheLeuProAspProGluAsnSerHisGlu

2470 2490 2510
CCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGCAGATCAA
ProSerSerHisProGluLysProLeuProAlaValSerProAspProGlnAlaAspGln

2530 2550 2570
GTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAA
ValGlnMetProArgSerCysLeuTrpEnd

2590 2610 2630
GACAGGTGGCCACTGACAGCCACTCCAGGAAGTTGAACTGCAGGGGCAGAGCCAGTGAAT

2650 2670 2690
CACCGGACCTCCAGCACCTGCAGGCAGCTTGGAAGTTTCTTCCCCGAGTGGAGCTTCGAC

2710 2730 2750
CCACCCACTCCAGGAACCCAGAGCCACACTAGAAGTTCCTGAGGGCTGGAGAACTGCT

2770 2790 2810
GGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCCCTG

2830 2850 2870
ACCTCCCTCACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCCAAAAGGGCTCTGTCTCTGGG

FIG. 5E

2890 2910 2930
AGTCTGGTGTGTCTCCTACATGCAATTTCCACGGACCCAGCTCTGTGGAGGGCATGACTG

2950 2970 2990
CTGGCCAGAAGCTAGTGGTCCTGGGGCCCTATGGTTCGACTGAGTCCACACTCCCCTGSA

3010 3030 3050
GCCTGGCTGGCCTCTGCAAACAAACATAATTTTGGGGACCTTCCTTCCTGTTTCTTCCCA

3070 3090 3110
CCCTGTCTTCTCCCCTAGGTGGTTCCTGAGCCCCACCCCCAATCCCAGTGCTACACCTG

3130 3150 3170
AGGTTCTGGAGCTCAGAATCTGACAGCCTCTCCCCCATCTGTGTGTGTGCGGGGGGACAG

3190 3210 3230
AGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGAAAGACATGTTGGCTATA

3250 3270 3290
GGCGTGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCYGGGGTAGGAGGATCACC

3310 3330 3350
AGAGGCCAGSAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAAAAA

3370 3390 3410
ATTTTAAAATTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTG

3430 3450 3470
AAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGGCACCCTG

3490 3510 3530
CACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAAGACATA

3550 3570

FIG. 5F

TTAA

FIG. 5G

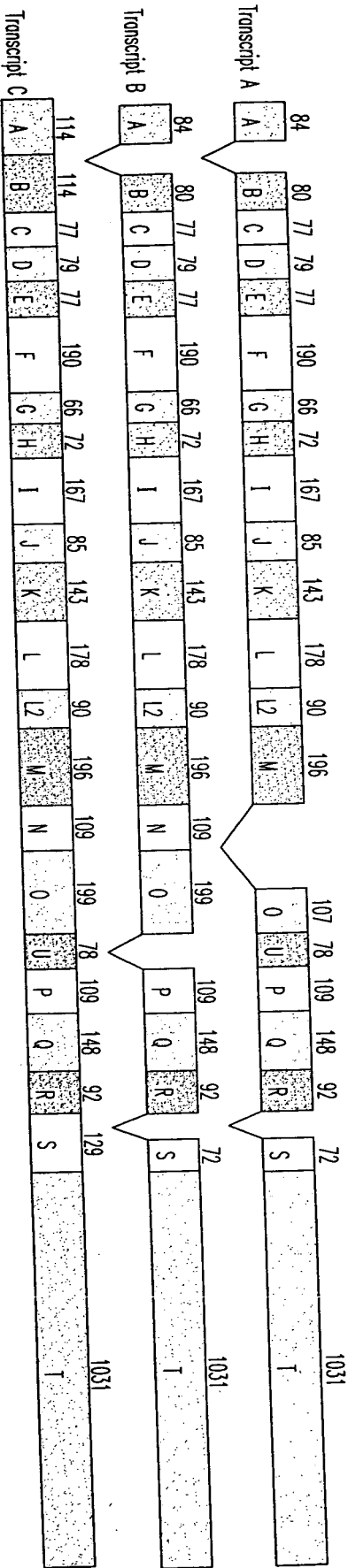


FIG. 6

>Gene216_A
ATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGG
CGCCGGGGTGCTTCAAG

>Gene216_B
GACATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCG

>Gene216_C
GTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCA

>Gene216_D
CAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCAGATGGGCAGCCAGTGGTGGTGGCCCCCAACCACAG

>Gene216_E
GATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAG

>Gene216_F
TGGCCTGATCACCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACCC
ACGAGATCTTTTCGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAGCGGGCATG
ACCAGCCTTCCTGGTGGTCCCCAGAGCAGG

>Gene216_G
GGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACACCCTG

>Gene216_H
TTCTTGACTCGGCACCGAAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTCGCCAACTACGTGGACCAG

>Gene216_I
CTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCGGCCTGGAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCA
GGACGCCAACGCCACGCTCTGGGCCTTCCTGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGGCCCCACGACTCCGCGCAGC
TGCTCAC

>Gene216_J
GGGCCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGA
GCACG

>Gene216_K
GACCACTCGGAGCTCCCCATCGGCGCCGCGAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCC
CGACGGCTGCTGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGG

>Gene216_L1
GCACCCGTTTCCGCGCGTGTTCAGCGCCTGCAGCCGCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCTTGCC
TCTCCAATGCCCCGGACCCCGGACTCCCGGTGCCGCGCGCGCTCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGT
GACTGCGGCCCCTGGCCAG

>Gene216_L2
GAGTGCCGCGACCTCTGCTGCTTTGCTCACAAGTCTGCTGCGTGGCCCCGGGGGGCCAGTGGCCCCACGGGGACTGCTGCGT
GCGCTGCCTG

>Gene216_M
CTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTTG:ACGGGCACCTCCTCCCA
CTGTCCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGAGTGGCTACTGCTGGGATGGCGCATGTCCCA
CGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCCTG

>Gene216_O

FIG. 7A

ATGGCCAGGAAGTGACTTGTCTGGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAG
CCAGGCACCCAGTGTGGACCTAGAATG

>Gene216_U_Alt
GTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGG

>Gene216_P
GTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAG
CATGGACAGTGGCCCTGTGCAGGCTGAAA

>Gene216_Q
ACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTCTGCTCCCAGGGGCGGCCTGGCCTGGTGTTC
TACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGG

>Gene216_R
CCCCAAAGATGGCCACACAGGGACCACCCCTGGGCGGCGTTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGC
CCTGGCCCCCTGG

>Gene216_S
ACCCTGAGAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAG

>Gene216_T
CAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGGCCA
CTGACAGCCACTCCAGGAACCTTGAAGTGCAGGGGCGAGGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGG
AAGTTTCTTCCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACACTAGAAGTTCTGAGGGCTGGAGA
ACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTACACAGCCCCCTGACCTCCCTCACC
AGTGGAGGCTGGGTAGTGCTGGCCATCCCAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCCTACATGCAATTTCCAC
GGACCCAGCTCTGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTCGACTGAGTCCACACT
CCCCTGGAGCCTGGCTGGCCTCTGCAAACAAACATAATTTGGGGACCTTCCTTCTGTTTCTTCCCACCCTGTCTTCTC
CCCTAGGTGGTTCTGAGCCCCCACCCTCAATCCAGTGCTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTC
CCCCATTCTGTGTGTGTCTGGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGAAAGACATGT
TGGCTATAGGCGTGGTGGCTCATGCCTATAATCCAGCACTTTGGGAAGCTGGGGTAGGAGGATCACCAGAGGCCAGGAG
GTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTTAAAATTAGCTGGGCGTGGTGGTGTGTA
CCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGG
CACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAGACATATTA

FIG. 7B

>Gene216_A
ATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGG
CGCCGGGGTGCTTCAAG

>Gene216_B
GACATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGSCGCACCGTCAGCCTGGAGGAGCCG

>Gene216_C
GTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCA

>Gene216_D
CAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCAGATGGGCAGCCAGTGGTGCTGGCCCCCAACCACAG

>Gene216_E
GATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAG

>Gene216_F
TGGCCTGATCACCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACCC
ACGAGATCTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAGCGGGCATG
ACCAGCCTTCCTGGTGGTCCCCAGAGCAGG

>Gene216_G
GGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACACCCTG

>Gene216_H
TTCTTGACTCGGCACCGAACTTGAACCACACCAACAGCGTCTCCTGGAAGTCGCCAACTACGTGGACCAG

>Gene216_I
CTTCTCAGGACTCTGGACATTCAAGTGGCGCTGACCGGCCTGGAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCA
GGACGCCAACGCCACGCTCTGGGCCTTCCTGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGC
TGCTCAC

>Gene216_J
GGGCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTGCAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGA
GCACG

>Gene216_K
GACCACTCGGAGCTCCCCATCGGCGCCGCGAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCC
CGACGGCTGCTGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGG

>Gene216_L1
GCACCCGTTTCCGCGCGTGTTCAGCGCCTGCAGCCGCCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCTTGCC
TCTCCAATGCCCCGACCCCGGACTCCCGGTGCCGCCGGCGCTCTGGGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGT
GACTGCGGGCCCTGGCCAG

>Gene216_L2
GAGTGCCGCGACCTCTGCTGCTTTGCTCACAAGTCTGCTGCGTGGCGCCGGGGGGCCAGTGCGCCACGGGGACTGCTGCGT
GCGCTGCCTG

>Gene216_M
CTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTGTG:ACGGGCACCTCCTCCCA
CTGTCCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGCGAGTGGCTACTGCTGGGATGGCGCATGTCCCA
CGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCCTG

FIG. 8A

>Gene216_N_Alt
GCTCCCACCCAGCTCCCAGGCCTGTTTCCAGGTGGTGAACCTCGCGGAGATGCTCATGGAACTGCGGCCAGGACAGC
GAGGGCCACTTCCTGCCCTGTGCAGGGAG

>Gene216_O_Alt
GGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTA
CCGTTTACCTAGATGGCCAGGAAGTGAAGTGTTCGGGGAGCCTTGGCACTCCCCAGTGGCAGCTGGACCTGCTTGGCCTG
GGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATG

>Gene216_P
GTTTGGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAG
CATGGACAGTGGCCCTGTGCAGGCTGAAA

>Gene216_Q
ACCATGACACCTTCCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTCTGCTCCCAGGGGCGGCCTGGCCTGGTGTTC
TACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGG

>Gene216_R
CCCCAAAGATGGCCCCACACAGGGACCACCCCTGGGCGGCGTTACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGC
CCTGGCCCCCTGG

>Gene216_S
ACCCTGAGAAGTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAG

>Gene216_T
CAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGGCCA
CTGACAGCCACTCCAGGAAGTGAAGTGCAGGGGCGAGGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGG
AAGTTTCTTCCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACACTAGAAGTTCCTGAGGGCTGGAGA
ACACTGCTGGGCACACTCTCCAGCTCAATAAAACCATCAGTCCCAGAAGCAAAGGTACACAGCCCCCTGACCTCCCTCACC
AGTGGAGGCTGGGTAGTGTGGCCATCCCAAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCCTACATGCAATTTCCAC
GGACCCAGCTCTGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCCTGGGGCCCTATGGTTGACTGAGTCCACACT
CCCCCTGGAGCCTGGCTGGCCTCTGCAAACAAACATAATTTTGGGGACCTTCCTTCCTGTTTCTTCCCACCCTGTCTTCTC
CCCTAGGTGGTTCCTGAGCCCCCACCCTCAATCCCAGTGTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTC
CCCCATTCTGTGTGTGTGCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAGACATGT
TGGCTATAGGCGTGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCTGGGGTAGGAGGATCACCAGAGGCCAGGAG
GTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAATTTTAAATTAGCTGGGCGTGGTGGTGTGTA
CCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAAGCTATGGTGG
CACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAGACATATTA

FIG. 8B

>Gene216_A_Alt
ATGGGCTGGAGGCCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGG
CGCCGGGGTGCTTCAAGGTGAGGACGCGGGCGGG

>Gene216_B_Alt
GTCCCCCTCACCTGTGCTCTGTCTTTACTCCAGGACATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTTGATGG
ACAACCTTGGCGCACCGTCAGCCTGGAGGAGCCG

>Gene216_C
GTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCA

>Gene216_D
CAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCAGATGGGCAGCCAGTGGTGTGGCCCCCAACCACAG

>Gene216_E
GATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAG

>Gene216_F
TGGCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACCC
ACGAGATCTTTCGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAGCGGGCATG
ACCAGCCTTCTGTGGTCCCCAGAGCAGG

>Gene216_G
GGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACACCCTG

>Gene216_H
TTCTTGACTCGGCACCGAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTCGCCAACTACGTGGACCAG

>Gene216_I
CTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCGGCCTGGAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCA
GGACGCCAACGCCACGCTCTGGGCCTTCTGTCAGTGGCGCCGGGGCTGTGGGCGCAGCGGGCCCCACGACTCCGCGCAGC
TGCTCAC

>Gene216_J
GGGCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTGGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGA
GCACG

>Gene216_K
GACCACTCGGAGCTCCCCATCGGCGCCGCGAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCC
CGACGGCTGCTGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGG

>Gene216_L1
GCAACCGTTTCCGCGCGTGTTACGCGCTGCAGCCGCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCTTGCC
TCTCCAATGCCCGGACCCCGGACTCCCGGTGCCGCGCGCTCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGT
GACTGCGGCCCTGGCCAG

>Gene216_L2
GAGTGCCGCGACCTCTGCTGCTTTGCTCACAAGTGTGCTGCGTGGCGCCGGGGGGCCAGTGGCGCCACGGGGACTGCTGCGT
GCGCTGCCTG

>Gene216_M
CTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTTG:ACGGGCACCTCCTCCCA
CTGTCCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGCGAGTGGCTACTGCTGGGATGGCGCATGTCCCA
CGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTG

FIG. 9A

>Gene216_N_Alt
GCTCCACCCAGCTCCCGAGGCTGTTTCCAGGTGGTGAAGTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGC
GAGGGCCACTTCTGCCCTGTGCAGGGAG

>Gene216_O_Alt
GGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTA
CCGTTCACTTAGATGGCCAGGAAGTGACTTGTGCGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTTGGCCTG
GGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATG

>Gene216_U_Alt
GTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGG

>Gene216_P
GTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAG
CATGGACAGTGGCCCTGTGCAGGCTGAAA

>Gene216_Q
ACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTCTGCTCCCAGGGGCGGCGCTGGCCTGGTGTGTC
TACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGG

>Gene216_R
CCCCAAAGATGCCCCACACAGGGACCACCCCCTGGGCGGCGTTACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGC
CCTGGCCCCCTGG

>Gene216_S_Alt
CCCCAGGGTCTCCTGCTGACCATATTCACAACATTTACCCTCCACCATTTCTCCCAGACCCTGAGAACTCTCATGAGCCC
AGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAG

>Gene216_T
CAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAAATGAACAGATTTAAAGACAGGTGGCCA
CTGACAGCCACTCCAGGAAGTTGAACTGCAGGGGCGAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGG
AAGTTTCTTCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACACTAGAAGTTCTGAGGGCTGGAGA
ACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCCCTGACCTCCCTCACC
AGTGGAGGCTGGGTAGTGTGCTGGCCATCCCAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCCTACATGCAATTTCCAC
GGACCCAGCTCTGTGAGGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTCGACTGAGTCCACACT
CCCCTGGAGCCTGGCTGGCCTCTGCAACAAACATAATTTGGGGACCTTCCTTCCTGTTTCTTCCACCCTGTCTTCTC
CCCTAGGTGGTTCTCTGAGCCCCCACCCTCAATCCAGTGCTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTC
CCCCATTCTGTGTGTGTGCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGAAAGACATGT
TGGCTATAGGCGTGGTGGCTCATGCCTATAATCCAGCACTTTGGGAAGCTGGGGTAGGAGGATCACCAGAGGCCAGGAG
GTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTTAAATTAGCTGGGCGTGGTGGTGTGTA
CCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGG
CACCCTGCACCTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAATAAATTTTAAAAAGACATATTA

FIG. 9B

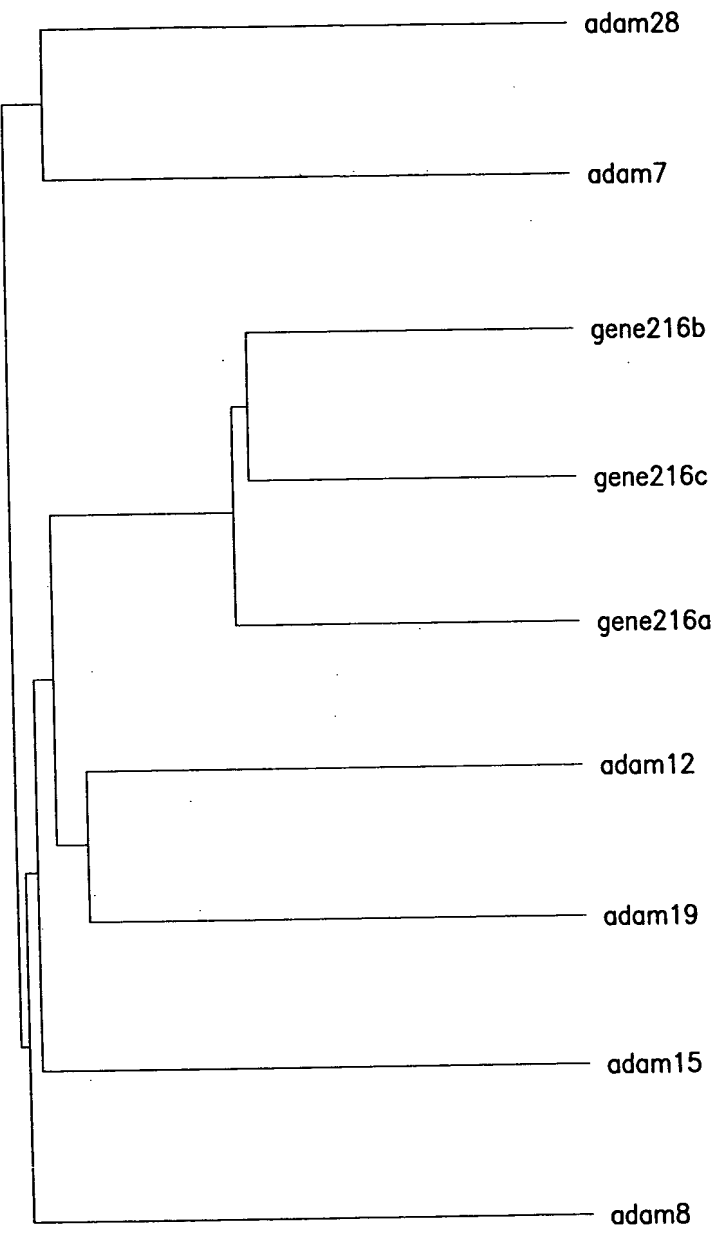


FIG. 10

		Signal sequence →						
		1				50		
adam28	M-----	-----LQG			LLPVSLLLSV	AVSAIKELPG		
adam7	-----	-----			-----	-----		
gene216b	MGWRPRRARG	TPLLLLLLLL	LLWPVPGAGV	LQ.....G			
gene216c	MGWRPRRARG	TPLLLLLLLL	LLWPVPGAGV	LQGEDAGGVP	LTLCSVFTPG			
gene216a	MGWRPRRARG	TPLLLLLLLL	LLWPVPGAGV	LQ.....G			
adam12	M-----	-----AARP			LPVSPARALL	LALAGALLAP	CEARGVSLWN	
adam19	-----	-----			-----	-----	-----	
adam15	M-----	-----RLALLW			ALGLLGAGSP	LPSWPLPNIG	GTEEQQAASE	
adam8	M-----	-----RGLG			LWLLGAMMLP	AIAPSRPWAL		
		Pro-domain →						
		51				100		
adam28	VKKYEVVYPI	RLHPLHKREA	KEPEQQEQFE	TELKYKMTIN	GKIAVLYLKK			
adam7	-----	-----			-----			
gene216b	HIPGQPVTPH	WVLDGQPWRT	VSLEEPVSKP	DMGLVALEAE	GQELLLLELEK			
gene216c	HIPGQPVTPH	WVLDGQPWRT	VSLEEPVSKP	DMGLVALEAE	GQELLLLELEK			
gene216a	HIPGQPVTPH	WVLDGQPWRT	VSLEEPVSKP	DMGLVALEAE	GQELLLLELEK			
adam12	EGRADDEVSA	SVRSGLDWIP	VKSFD SKNHP	EVLNIRLQRE	SKELIINLER			
adam19	-----	-----			-----			
adam15	KAPREPLEPQ	VLQDDL.P.IS	LKKVLQTSLP	EPLRIKLELD	GDSHILELLQ			
adam8	MEQYEVVLP	RLPGPRVRR	LPSHLGL.HP	ERVS YVLGAT	GHNFTLHLRK			
		101				150		
adam28	NKNLLAPGYT	ETYYNSTGKE	ITTSP...QI	MDDCYQGHI	LNEKVS DASI			
adam7	-----	-----			-----			
gene216b	NHRLAPGYI	ETHYGPDGQP	VVLAPNHT..	.DHCHYQGRV	RGFPDSWVVL			
gene216c	NHRLAPGYI	ETHYGPDGQP	VVLAPNHT..	.DHCHYQGRV	RGFPDSWVVL			
gene216a	NHRLAPGYI	ETHYGPDGQP	VVLAPNHT..	.DHCHYQGRV	RGFPDSWVVL			
adam12	NEGLIASSFT	ETHYLQDGT	VSLARNYTVI	LGH CYHGHV	RGYSDSAVSL			
adam19	-----	-----S			GNPQTTRKL	EDHCFYHGT	RETELSSVTL	
adam15	NRELVPGRPT	LVWYQPDGTR	VV...SEGHT	LENCCYQGRV	RGYAGSWVSI			
adam8	NRDLLGSGYT	ETYTAANGSE	VTEQP...RG	QDHCLYQGHV	EGYPDSAASL			
		Cysteine switch					200	
adam28	STCRGLRGYF	SQG.DQRYFI	EPLSPIHRDG	QEHALFKYNP	DEKNYDSTCG			
adam7	-----	-----			-----			
gene216b	CTCSGMSGLI	TLSRNASYYL	RPWPPRGSKD	FSTHEIFRME	QLLTWKGTCG			
gene216c	CTCSGMSGLI	TLSRNASYYL	RPWPPRGSKD	FSTHEIFRME	QLLTWKGTCG			
gene216a	CTCSGMSGLI	TLSRNASYYL	RPWPPRGSKD	FSTHEIFRME	QLLTWKGTCG			
adam12	STCSGLRGLI	.VFENESYVL	EPMKSATNR.	...YKLFPK	KLKSVRGSCG			
adam19	STCRGIRGLI	TVSSNLSYVI	EPLPDSKGQ.	...HLIYRSE	HLKPPPGNCG			
adam15	CTCSGLRGLV	VLTPERSYTL	EQGP...GDL	QGPPIIISRIQ	DLHLPGHTCA			
adam8	STCAGLRGFF	QVGSDL.HLI	EPLDEGG..E	GGRHAVYQAE	HLLQTAGTCG			
		201				Catalytic domain		
adam28	MDGVLWAHDL	QQNIALPATK	LV.KLKDRKV	QEHEKYIEYY	LVLDNGEFKR			
adam7	-NYSCTELNF	TRKTVPGDNE	SE.EDSKIKG	IHDEKYVELF	IVADDTVYRR			
gene216b	..HRDPGNKA	GMTSLPGGPQ	SRGRREARRT	...RKYLELY	IVADHTLFLT			
gene216c	..HRDPGNKA	GMTSLPGGPQ	SRGRREARRT	...RKYLELY	IVADHTLFLT			
gene216a	..HRDPGNKA	GMTSLPGGPQ	SRGRREARRT	...RKYLELY	IVADHTLFLT			
adam12	SHHNTPNLAA	KNV.FPPPSQ	TWARRHKRET	LKATKYVELV	IVADNREFQR			
adam19	FEHSKPPTTD	WALQFTQQT	KRPRRMKRED	LNSMKYVELV	LVADYLEFQK			
adam15	LSWRESVHTQ	TPPEHPLGQR	HIRRR..RDV	VTETKYVELV	IVADHSE.AQ			
adam8	VSDDSLGSLL	GPRT...AAV	FRPRPGDSL	SRETRYVELY	VVVDNAEFQM			

	251				300
adam28	YNENQDEIRK	RVFEMANYVN	MLYKKLNTHV	ALVGMEIWD	KDKIKITPNA
adam7	NGHPHNKLRL	RIWGMVNFVN	MIYKTLNIHV	TLVGIEIWDH	EDKIELYSNI
gene216b	RHRNLNHTKQ	RLLEVANYVD	QLLRTLDIQV	ALTGLEVWTE	RDRSRVTQDA
gene216c	RHRNLNHTKQ	RLLEVANYVD	QLLRTLDIQV	ALTGLEVWTE	RDRSRVTQDA
gene216a	RHRNLNHTKQ	RLLEVANYVD	QLLRTLDIQV	ALTGLEVWTE	RDRSRVTQDA
adam12	QGKDLEKVKQ	RLIEIANHVD	KFYRPLNIRI	VLVGVEVWND	MDKCSVSQDP
adam19	NRRDQDATKH	KLIEIANYVD	KFYRSLNIRI	ALVGLEVWTH	GNMCEVSENP
adam15	KYRDFQHLLN	RTLEVALLLD	TFFRPLNVRV	ALVGLEAWTQ	RDLVEISPNP
adam8	LGSEA.AVRH	RVLEVNVHVD	KLYQKLNFRV	VLVGLEIWN	QDRFHVSPDP
	301				350
adam28	SFTLENFSKW	RGSVLSRRKR	HDIAQLITAT	ELAGTTVGLA	FMSTMCS.P.Y
adam7	ETTLRLFSFW	QEKILKTRKD	FDHVVLLSGK	WLYSHVQGIS	YPGGMCLPYY
gene216b	NATLWAFLOW	RRG.LWAQRP	HDSAQLLTGR	AFQGATVGLA	PVEGMCRAES
gene216c	NATLWAFLOW	RRG.LWAQRP	HDSAQLLTGR	AFQGATVGLA	PVEGMCRAES
gene216a	NATLWAFLOW	RRG.LWAQRP	HDSAQLLTGR	AFQGATVGLA	PVEGMCRAES
adam12	FTSLHEFLDW	RKMKLLPRKS	HDNAQLVSGV	YFQGTIGMA	PIMSMCTADQ
adam19	YSTLWSFLSW	RR.KLLAQKY	HDNAQLITGM	SFHGTTIGLA	PLMAMCSVYQ
adam15	AVTLENFLHW	RRAHLLPRLP	HDSAQLVTGT	SFSGPTVGMA	IQNSICSPDF
adam8	SVTLENLLTW	QARQTRRHL	HDNVQLITGV	DFTGTTVGFA	RVSAMCS.HS
	351		Metalloprotease domain		400
adam28	SVGVVDHSD	NLLRVAGTMA	HEMGNHFGMF	HDDYSCKC..PSTICV
adam7	STSIKDLLP	DTNIIANRMA	HQLGHNLMGQ	HDEFPTC..PSGKCV
gene216b	SGGVSTDHSE	LPIGAAATMA	HEIGHSLGLS	HD..PDGCCV	EAAAESGGCV
gene216c	SGGVSTDHSE	LPIGAAATMA	HEIGHSLGLS	HD..PDGCCV	EAAAESGGCV
gene216a	SGGVSTDHSE	LPIGAAATMA	HEIGHSLGLS	HD..PDGCCV	EAAAESGGCV
adam12	SGGIVMDHSD	NPLGAAVTLA	HELGNHFGMN	HDTLDRGCSC	QMAVEKGGCI
adam19	SGGVNMDHSE	NAIGVAATMA	HEMGNHFGMT	HDSAD...CC	SASAADGGCI
adam15	SGGVNMDHST	SILGVASSIA	HELGHSLGLD	HDLPGNSPCP	PGPAPAKTCI
adam8	SGAVNQDHSK	NPVGVACTMA	HEMGNHLMGD	HDENVQGCRC	QERFEAGRCI
	"Met-turn"				450
adam28	MDKALSFIYP	TDFSSCSRLS	YDKFFEDKLS	NCLFNAPLPT	DIISTPICGN
adam7	MDSDGSI.PA	LDLSKCRQNO	YHQYLKDYKP	TCMLNIPFPY	NFHDFQFCGN
gene216b	MAAATGHFPF	RVFSACSRRQ	LRAFFRKGGG	ACLSNAPDPG	LPVPPALCGN
gene216c	MAAATGHFPF	RVFSACSRRQ	LRAFFRKGGG	ACLSNAPDPG	LPVPPALCGN
gene216a	MAAATGHFPF	RVFSACSRRQ	LRAFFRKGGG	ACLSNAPDPG	LPVPPALCGN
adam12	MNASTGYFPF	MVFSSCSRKD	LETSLEKGMG	VCLFNLPFVR	ESFGGQCKGN
adam19	MAAATGHFPF	KVFNGCNRR	LDRLYQSGGG	MCLSNMPDTR	MLYGGRRCCGN
adam15	MEASTDFLPG	LNFSNCSRRA	LEKALLDGMG	SCLFERL.PS	PLPMAAFCCGN
adam8	MAGSIGSSFP	RMFSDCSQAY	LESFLERPQS	VCLANAPDLS	HLVGGPVCCGN
	451		Disintegrin domain		500
adam28	QLVEMGEDCD	CGTSEECTNI	CCDAKTCKIK	ATFQCAL.GE	CCEKCQFKKA
adam7	KKLDEGEECD	CGPAQECTNP	CCDAHTCVLK	PGFTCAE.GE	CCESCQIKKA
gene216b	GFVEAGEECD	CGPGQECDL	CCFAHNCSLR	PGAQCA.HGD	CCVRCCLKPA
gene216c	GFVEAGEECD	CGPGQECDL	CCFAHNCSLR	PGAQCA.HGD	CCVRCCLKPA
gene216a	GFVEAGEECD	CGPGQECDL	CCFAHNCSLR	PGAQCA.HGD	CCVRCCLKPA
adam12	RFVEEGECD	CGEPEECMNR	CCNATTCTLK	PDAVCA.HGL	CCEDCQLKPA
adam19	GYLEDEGECD	CGEEECNNP	CCNASNCTLR	PGAECA.HGS	CCHQCKLLAP
adam15	MFVEPGEQCD	CGFLDDCVDP	CCDSLTCQLR	PGAQCASDGP	CCQNCQLRPS
adam8	LFVERGEQCD	CGPPEDCRNR	CCNSTTCQLA	EGAQCA.HGT	CCQECKVKPA

	501				550
adam28	GMVCRPAKDE	CDLPEMCNGK	SGNCPDDRFO	VNGFPCHHGK	GHCLMGTCPT
adam7	GSICRPAKDE	CDFPEMCTGH	SPACPKDQFR	VNGFPCKNSE	GYCFMGKCPT
gene216b	GALCRQAMGD	CDLPEFCTGT	SSHCPEDVYL	LDGSPCARGS	GYCWDGACPT
gene216c	GALCRQAMGD	CDLPEFCTGT	SSHCPEDVYL	LDGSPCARGS	GYCWDGACPT
gene216a	<u>GALCRQAMGD</u>	<u>CDLPEFCTGT</u>	<u>SSHCPEDVYL</u>	LDGSPCARGS	GYCWDGACPT
adam12	GTACRDSSNS	CDLPEFCTGA	SPHCPANVYL	HDGHSCQDVD	GYCYNGICQT
adam19	GTLCREQARQ	CDLPEFCTGK	SPHCPTNFYQ	MDGTPCEGGQ	AYCYNGMCLT
adam15	GWQCRPTRGD	CDLPEFCPGD	SSQCPPDVSL	GDGEPCAGGQ	AVCMHGRCAS
adam8	GELCRPKKDM	CDLEEFCDGR	HPECPEDAFQ	ENGTPCSGG.	.YCYNGACPT
Cysteine rich domain					
					600
adam28	LQEQCTELWG	PGTEVADKSC	YNR.NEGGSK	YGYC.RRVDD	TLIPCKANDT
adam7	REDQCSELF	DEAIESHDIC	YKM.NTKGNK	FGYC.KNKEN	RFLPCEEKDV
gene216b	LEQQCQQLWG	PGSHPAPEAC	FQVVNSAGDA	HGNCGQDSEG	HFLPCAGRDA
gene216c	LEQQCQQLWG	PGSHPAPEAC	FQVVNSAGDA	HGNCGQDSEG	HFLPCAGRDA
gene216a	LEQQCQQLWG	P.....
adam12	HEQQCVTLWG	PGAKPAPGIC	FERVNSAGDP	YGNCGKVSks	SFAKCEMRDA
adam19	YQEQCQQLWG	PGARPAPDLC	FEKVNvagdt	FGNCGKVMNG	EHRKCNMRDA
adam15	YAQQCQSLWG	PGAQPAAPLC	LQTANTRGNA	FGSCGRNPSG	SYVSCTPRDA
adam8	LAQQCQAFWG	PGGQAAEESC	FsyDILPG..CKASRYRAD
	601				650
adam28	MCGKLFCQGG	S.DNLPPWKGR	..IV.....	..TFLTCKTFDPED
adam7	RCGKIYCTGG	ELSSLLGEDK	..TYHLKDPQ	KNATVKCKTIFLYH
gene216b	LCGKLQCQGG	KP.SLLAPHM	VPVDSTVHL.	DGQEVTCRGA	LAL..PSAQL
gene216c	LCGKLQCQGG	KP.SLLAPHM	VPVDSTVHL.	DGQEVTCRGA	LAL..PSAQL
gene216a	DGQEVTCRGA	LAL..PSAQL
adam12	KCGKIQCQGG	ASRPVIGTNA	VSIETNIPLQ	QGGRILCRGT	HVYLG....D
adam19	KCGKIQCQSS	EARP.LESNA	VPIDTTI.IM	NGRQIQCRGT	HVYRGPEEEG
adam15	ICGQLQCQTG	RTQPLLGSIR	DLLWETIDV.	NGTELNCswv	HLDLGS....
adam8	MCGVLQCKGG	QQPLGRAICI	VDVCHALTTE	DGTAYE....
EGF-like domain					
	651				700
adam28	TSQEIGMVAN	GTKCGDNKVC	INAECVDIEK	AYKSTNCSSK	CKGHAVCDHE
adam7	DSTDIGLVAS	GTKCGEGMVC	NNGECLNMEK	VYISTNCPSQ	CNENPVDGHG
gene216b	DLLGLGLVEP	GTQCGPRM..VCNSN.
gene216c	DLLGLGLVEP	GTQCGPRMVC	QSRRCRKNA.	FQELQRCLTA	CHSHGVCNSN
gene216a	DLLGLGLVEP	GTQCGPRMVC	QSRRCRKNA.	FQELQRCLTA	CHSHGVCNSN
adam12	DMPDPGLVLA	GTKCADGKIC	LNRQCQNIS.	VFGVHECAMQ	CHGRGVCNNR
adam19	DMLNPGLVMT	GTKCGYNHIC	FEGQCRNTS.	FFETEGCGKK	CNGHGVCNNN
adam15	DVAQPLLTLT	GTACGPGLVC	IDHRCQRVD.	LLGAQECSRK	CHGHGVCDSN
adam8PVPE	GTRCGPEKVC	WKGRCDLH.	VYRSSNCSAQ	CHNHGVCNHNK
Transmembrane					
	701				
adam28	LQCQCEEGWI	PPDCDDSSVV	FHFSIVVGVL	FPMaVIFVVV	AMVIRHQSSR
adam7	LQCHCEEGQA	PVACEETLHV	TNITILVVVL	VLVIVGIGVL	<u>ILLVRYRKCI</u>
gene216b	HNCHCAPGWA	PPFCDKPGFG	GSMD.SGPVQ	AENHDTFLLA	<u>MLLSVLLPLL</u>
gene216c	HNCHCAPGWA	PPFCDKPGFG	GSMD.SGPVQ	AENHDTFLLA	<u>MLLSVLLPLL</u>
gene216a	HNCHCAPGWA	PPFCDKPGFG	GSMD.SGPVQ	AENHDTFLLA	<u>MLLSVLLPLL</u>
adam12	KNCHCEAHWA	PPFCDKPGFG	GSTD.SGPIR	QAEARQEAAE	SNRERGQOQE
adam19	QNCHCLPGWA	PPFCNTPGHG	GSID.SGPM.	PPESVGPVVA	GVLVAILVLA
adam15	RHCYCEEGWA	PPDCTTQLKA	TSSL.TTGLL	L.SLLVLLVL	VMLGAGYWYR
adam8	QECHCHAGWA	PPHCAKLLTE	VHAA.SGSLP	VLVVVVVLVLL	AVVLVTLAGI

FIG. 11C

	Domain →	Cytoplasmic domain →				800
adam28	EKQKKDQRPL	STTGTRPHKQ	KRKPQMVKAV	QPQEMSQMKP	HVYDLPVEGN	
adam7	KLKQVQSPPT	ETLGVENKGY	FGDEQQIRTE	PILPEIHFLN	KPASKDSRGI	
gene216b	PGAGLAWCCY	RLPGAHLQRC	SWGCRDPAC	SGPKDGPHRD	HPLGGVHPME	
gene216c	PGAGLAWCCY	RLPGAHLQRC	SWGCRDPAC	SGPKDGPHRD	HPLGGVHPME	
gene216a	PGAGLAWCCY	RLPGAHLQRC	SWGCRDPAC	SGPKDGPHRD	HPLGGVHPME	
adam12	PVGSQEHAST	ASLTLI----	-----	-----	-----	
adam19	VLMLMYCCCR	QNNKLGQLKP	SALPSKLRQQ	FSCPFRVSQN	SGTGHANPTF	
adam15	ARLHQRLCQL	KGPTCQYRAA	QSGPSERPGP	PQRALLARGT	KSQGPAPKPPP	
adam8	IVYRKARSRI	LSRNVAPKTT	MGRSNPLFHQ	AASRVPAKGG	APAPSRGPQE	
	801					
adam28	EPPASFHKDT	NALPPTVFKD	NPMSTPKDSN	PKA-----	Putative SH ₃	
adam7	ADPNQSAK--	-----	-----	-----	-----	
gene216b	LGPTATGQPW	PL.....DPENSHEPS	SHPEKPLPAV	
gene216c	LGPTATGQPW	PLAPGSPADH	IHNIYPPPFLL	PDPENSHEPS	SHPEKPLPAV	
gene216a	LGPTATGQPW	PL.....DPENSHEPS	SHPEKPLPAV	
adam12	-----	-----	-----	-----	-----	
adam19	KLQTPQGKRK	VINTPEILRK	PSQPPPRPPP	DYLRGGSPPA	PLPAHLSRAA	
adam15	PRKPLPADPQ	GRCPSGDLPG	PGAGIPPLVV	PSRPAPPPPT	VSSLYL----	
adam8	LVPTTHPGQP	ARHPASSVAL	KRPPPAPPVT	VSSPPFPVPV	YTRQAPKQVI	
	851					
	binding domain					900
adam28	-----	-----	-----	-----	-----	
adam7	-----	-----	-----	-----	-----	
gene216b	SPDPQADQVQ	MPRSCLW----	-----	-----	-----	
gene216c	SPDPQADQVQ	MPRSCLW----	-----	-----	-----	
gene216a	SPDPQADQVQ	MPRSCLW----	-----	-----	-----	
adam12	-----	-----	-----	-----	-----	
adam19	RNSPGPGSQI	ERTESSRRPP	PSRPIPPAPN	CIVSQDFSRL	RPPQKALPAN	
adam15	-----	-----	-----	-----	-----	
adam8	KPTFAPPVPP	VKPGAGAANP	GPAEGAVGPK	VALKPPIQRK	QGAGAPTAP--	
	901					
adam28	-----	-----	-----	-----	-----	
adam7	-----	-----	-----	-----	-----	
gene216b	-----	-----	-----	-----	-----	
gene216c	-----	-----	-----	-----	-----	
gene216a	-----	-----	-----	-----	-----	
adam12	-----	-----	-----	-----	-----	
adam19	PVPGRRLPR	PGGASPLRPP	GAGPQOSRPL	AALAPKVSPR	EALKVKAGTR	
adam15	-----	-----	-----	-----	-----	
adam8	-----	-----	-----	-----	-----	
	951					
adam28	-----	-----	-----	-----	-----	
adam7	-----	-----	-----	-----	-----	
gene216b	-----	-----	-----	-----	-----	
gene216c	-----	-----	-----	-----	-----	
gene216a	-----	-----	-----	-----	-----	
adam12	-----	-----	-----	-----	-----	
adam19	GLQGGRCRVE	GTKQFMLLVV	WTELPEQKPR	AKHSCFLVPA	-----	
adam15	-----	-----	-----	-----	-----	
adam8	-----	-----	-----	-----	-----	
	990					

FIG. 11D

mGene216	MGSRCGRPGG	SPVLLLLPLL	LPSCLRSAR	MFPASIPKPH	LHIPTCTWLT	50	
Gene 216c	MGWR	-----	-----	-----	-----	12	
Gene 216b	MGWR	-----	-----	-----	-----	12	
Gene 216a	MGWR	-----	-----	-----	-----	12	
mGene216	NYEAHVTLRT	RFLLELLFQI	LKMYMSVLPA	HASVYRGNA	HG-----	92	
Gene 216c	-----	L-LLLLLL	LLIW--FVPG	-AGVLQ-GED	AGGVPLTLCS	45	
Gene 216b	-----	L-LLLLLL	LLIW--FVPG	-AGVLQ-GHI	FG-----	37	
Gene 216a	-----	L-LLLLLL	LLIW--FVPG	-AGVLQ-GHI	FG-----	37	
mGene216	-----	E-LVTPHWILEG	RLWLKVTLEE	PILKPD	SVLV-ALEAEGQDLL	133	
Gene 216c	VFTPGHIPGQ	FVTTPHWVLDG	QFWRTVSLEE	PVSKPD	MGLV-ALEAEGQELL	95	
Gene 216b	-----	Q-FVTTPHWVLDG	QFWRTVSLEE	PVSKPD	MGLV-ALEAEGQELL	78	
Gene 216a	-----	Q-FVTTPHWVLDG	QFWRTVSLEE	PVSKPD	MGLV-ALEAEGQELL	78	
mGene216	LELEKKHKLL	APGYIETHYR	PDGHPVVLSP	NHTDHCQYHG	RVRGFRESWV	183	
Gene 216c	LELEKNHRLL	APGYIETHYG	PDGQPVVLAP	NHTDHCYQG	RVRGFEDSWV	145	
Gene 216b	LELEKNHRLL	APGYIETHYG	PDGQPVVLAP	NHTDHCYQG	RVRGFEDSWV	128	
Gene 216a	LELEKNHRLL	APGYIETHYG	PDGQPVVLAP	NHTDHCYQG	RVRGFEDSWV	128	
mGene216	VLTCSGMSG	LITLSRNASY	YLRFPWPPRG	KDFSTHEIFR	MEQLITWKGT	233	
Gene 216c	VLTCTSGMSG	LITLSRNASY	YLRFPWPPRG	KDFSTHEIFR	MEQLITWKGT	195	
Gene 216b	VLTCTSGMSG	LITLSRNASY	YLRFPWPPRG	KDFSTHEIFR	MEQLITWKGT	178	
Gene 216a	VLTCTSGMSG	LITLSRNASY	YLRFPWPPRG	KDFSTHEIFR	MEQLITWKGT	178	
mGene216	QRDKNSOYKA	GMASLEHVPQ	SRVRREARRS	RYLELYIVA	DHTLV----	278	
Gene 216c	CGHRDPCNKA	GMTSLGGEQ	SRGRREARRT	RKYLELYIVA	DHTLFLTRHR	245	
Gene 216b	CGHRDPCNKA	GMTSLGGEQ	SRGRREARRT	RKYLELYIVA	DHTLFLTRHR	228	
Gene 216a	CGHRDPCNKA	GMTSLGGEQ	SRGRREARRT	RKYLELYIVA	DHTLFLTRHR	228	
mGene216	SPSDSD	---SGY---	TVGVDRAG	SVD-RAGSOS	HHSGRKRNA-	314	
Gene 216c	NLNHTIKORLL	EVANYVDQLL	RTLDIQVALT	GLEVWTERDR	SRVTQDANAT	295	
Gene 216b	NLNHTIKORLL	EVANYVDQLL	RTLDIQVALT	GLEVWTERDR	SRVTQDANAT	278	
Gene 216a	NLNHTIKORLL	EVANYVDQLL	RTLDIQVALT	GLEVWTERDR	SRVTQDANAT	278	
mGene216	L-GF-----	-----PT---	---VAFR---	G---VG---	QE-TTRLHTT---	335	
Gene 216c	LWAFLOWRRG	LWAQRPHDSA	QLLTGRAFCG	ATVGLAPVEG	MCRABSSGGV	345	
Gene 216b	LWAFLOWRRG	LWAQRPHDSA	QLLTGRAFCG	ATVGLAPVEG	MCRABSSGGV	328	
Gene 216a	LWAFLOWRRG	LWAQRPHDSA	QLLTGRAFCG	ATVGLAPVEG	MCRABSSGGV	328	
mGene216	AHDHSELPIG	TAATMAHEIG	HSLGLSHDPD	GCCVQADAEQ	GGCVMEAAATG	385	
Gene 216c	STDHSELPIG	AAATMAHEIG	HSLGLSHDPD	GCCVEAAAES	GGCVMAAATG	395	
Gene 216b	STDHSELPIG	AAATMAHEIG	HSLGLSHDPD	GCCVEAAAES	GGCVMAAATG	378	
Gene 216a	STDHSELPIG	AAATMAHEIG	HSLGLSHDPD	GCCVEAAAES	GGCVMAAATG	378	
mGene216	HPFPRVFSAC	SRRLRTFFR	KGGGCLSNT	SAPGLVLP	RCNGFLEAG	435	
Gene 216c	HPFPRVFSAC	SRRLRAFFR	KGGGACLSNA	PDPGLVPPA	LCNGFVEAG	445	
Gene 216b	HPFPRVFSAC	SRRLRAFFR	KGGGACLSNA	PDPGLVPPA	LCNGFVEAG	428	
Gene 216a	HPFPRVFSAC	SRRLRAFFR	KGGGACLSNA	PDPGLVPPA	LCNGFVEAG	428	
mGene216	EECDCGSGQ	-----	-----	-----	L-KSAGT	PCRA	455
Gene 216c	EECDCGPGQE	CRDLCCFAHN	CSLRPGAQCA	HGDCCVRCIL	KPAGALCROA	495	
Gene 216b	EECDCGPGQE	CRDLCCFAHN	CSLRPGAQCA	HGDCCVRCIL	KPAGALCROA	478	
Gene 216a	EECDCGPGQE	CRDLCCFAHN	CSLRPGAQCA	HGDCCVRCIL	KPAGALCROA	478	

FIG. 12A

mGene216	ATDCDLPEFC	TGTSPYCPAD	VYLLDGSPCA	EGRGYCLDGW	CPTLEQQCQQ	505	
Gene 216c	MGDCDLPEFC	TGTSSHCPPD	VYLLDGSPCA	RGSGYCWDCG	CPTLEQQCQQ	545	
Gene 216b	MGDCDLPEFC	TGTSSHCPPD	VYLLDGSPCA	RGSGYCWDCG	CPTLEQQCQQ	528	
Gene 216a	MGDCDLPEFC	TGTSSHCPPD	VYLLDGSPCA	RGSGYCWDCG	CPTLEQQCQQ	528	
mGene216	LWGPFGSKPAP	EPCFQOMNSM	GNSQGNCGQD	HKGSFLPCAQ	RDALCGKLLC	555	
Gene 216c	LWGPFGSHPAP	EACFQVVNSA	GDAHGNCGQD	SEGHFLPCAG	RDALCGKLQC	595	
Gene 216b	LWGPFGSHPAP	EACFQVVNSA	GDAHGNCGQD	SEGHFLPCAG	RDALCGKLQC	578	
Gene 216a	LWGHDGQ---	-----	-----	-----	-----	535	
mGene216	QGGEPNPLVP	HIVTMDSTIL	LEGREVVCRG	AFVLPDSHLD	QLDLGLVEPG	605	
Gene 216c	QGGKPSLLAP	HMVPVDSTVH	LDGQEVTCRG	ALALPSAQLD	LLGLGLVEPG	645	
Gene 216b	QGGKPSLLAP	HMVPVDSTVH	LDGQEVTCRG	ALALPSAQLD	LLGLGLVEPG	628	
Gene 216a	-----	-----	-----EVT	CRG ALALPSAQLD	LLGLGLVEPG	561	
mGene216	TQCGPRM---	-----	-----	-----	-----P	613	
Gene 216c	TQCGPRMVCQ	SRRCRKNAFQ	ELQRCLTACH	SHGVCNSNHN	CHCAPGWAPP	695	
Gene 216b	TQCGPRMVCN	SNHNCHCA--	-----	-----	-----PGWAPP	652	
Gene 216a	TQCGPRMVCQ	SRRCRKNAFQ	ELQRCLTACH	SHGVCNSNHN	CHCAPGWAPP	611	
mGene216	--HGP	LANS	VRTLHLITCS	QT--LRTL	SL PKNYPL	-----KCP	647
Gene 216c	FCDKPGFGGS	MDSGEVQAEH	HDTEILLAMLL	SVLLPL	-----	-----LP	733
Gene 216b	FCDKPGFGGS	MDSGEVQAEH	HDTEILLAMLL	SVLLPL	LPGA	GLAWCCYRIP	702
Gene 216a	FCDKPGFGGS	MDSGEVQAEH	HDTEILLAMLL	SVLLPL	LPGA	GLAWCCYRIP	661
mGene216	GLQIEF---	-----	-----QTC	-PI--PMRED	K-CAL-PCDL	671	
Gene 216c	GAGLAWCCYR	LPGAHLQRC	WGCRDRFACS	GPKDGEHRDH	PLGGVHEMEL	783	
Gene 216b	GAHLQRC---	-----S	WGCRDRFACS	GPKDGEHRDH	PLGGVHEMEL	740	
Gene 216a	GAHLQRC---	-----S	WGCRDRFACS	GPKDGEHRDH	PLGGVHEMEL	699	
mGene216	-QSSVSQT--	-----	-----	HSYNSY--GL	YAEILL	SIGT	696
Gene 216c	GPTATGQWPW	LAPGSPADHI	HNIYPPPFLLP	DPENSHEPSS	HPEKFLPAVS	833	
Gene 216b	GPTATGQWPW	L-----	-----	DPENSHEPSS	HPEKFLPAVS	771	
Gene 216a	GPTATGQWPW	L-----	-----	DPENSHEPSS	HPEKFLPAVS	730	
mGene216	PEP--DHV--V--SR--LP					707	
Gene 216c	PDPQADQVQM	PRSCILW				849	
Gene 216b	PDPQADQVQM	PRSCILW				787	
Gene 216a	PDPQADQVQM	PRSCILW				746	

FIG. 12B

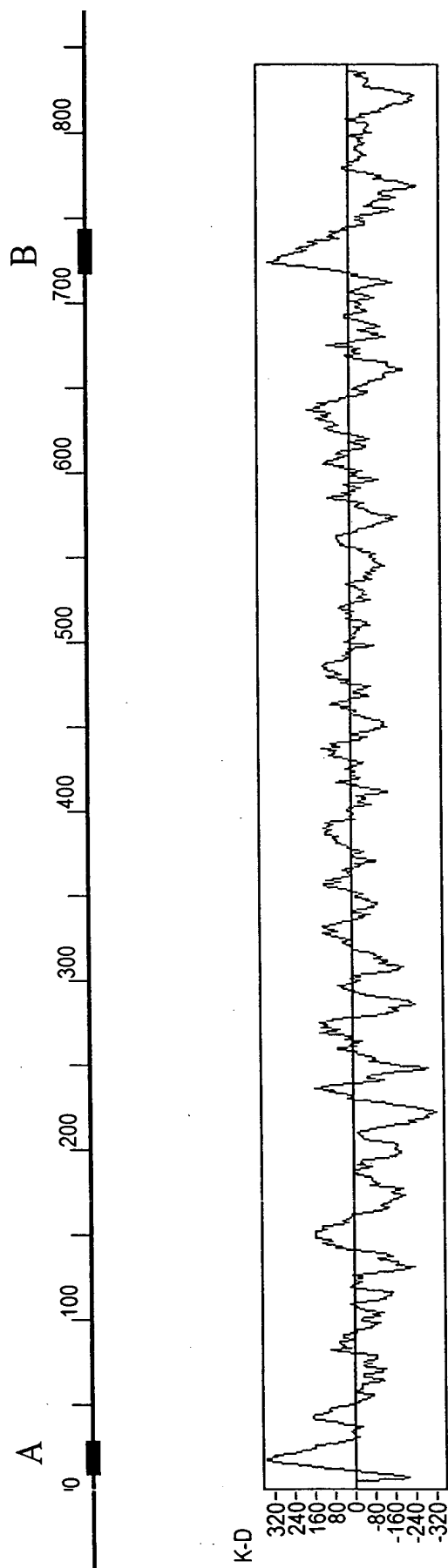


FIG. 13

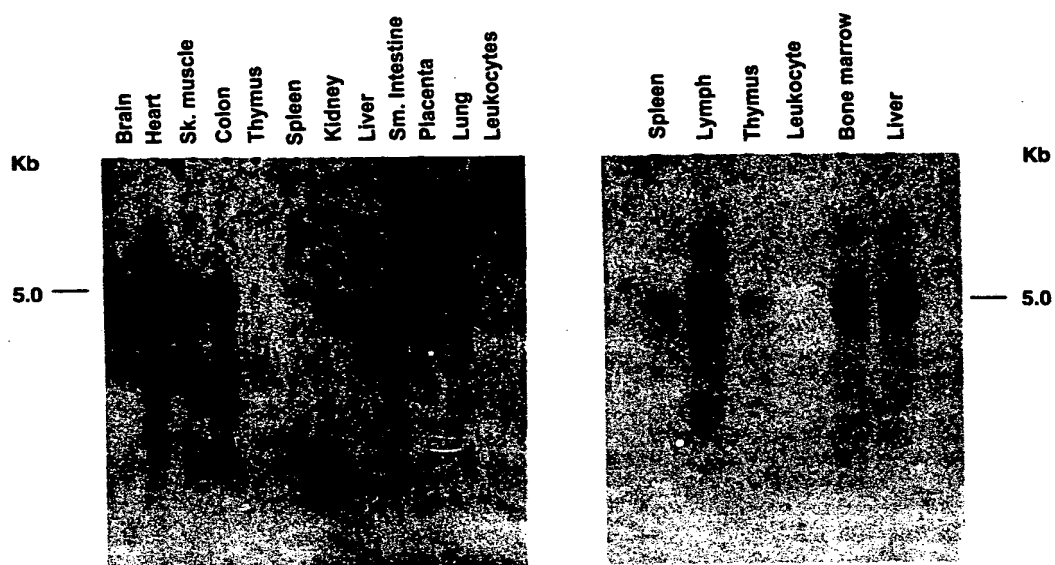


FIG. 14

Gene_216: Transcript A

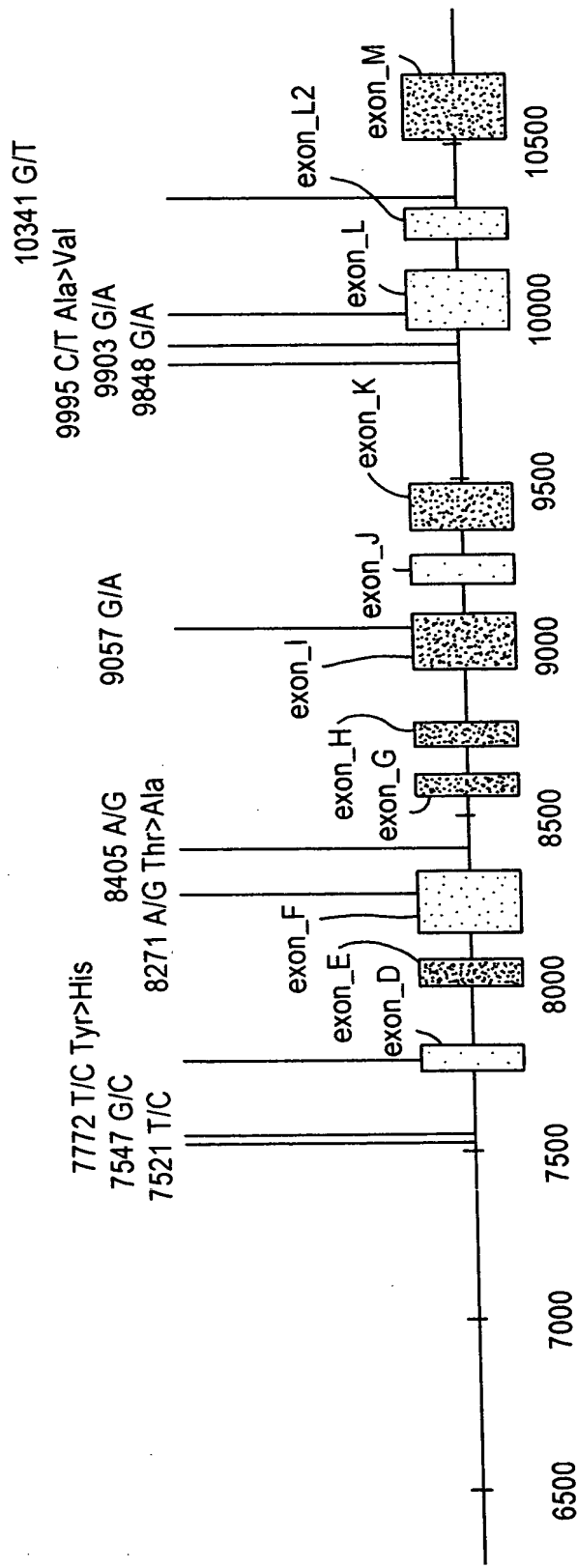
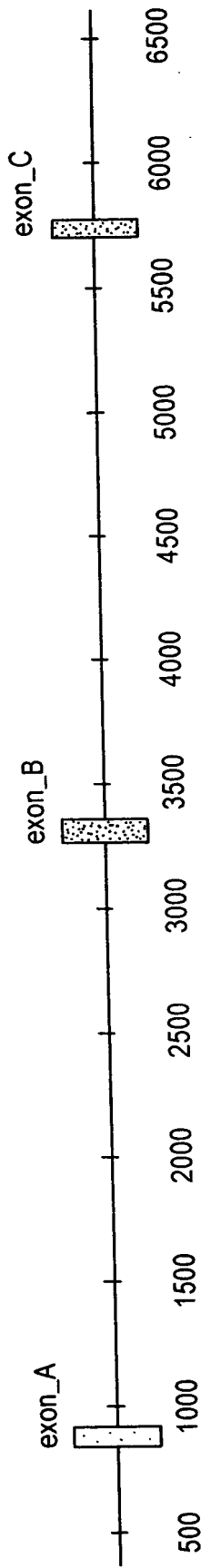


FIG. 15A

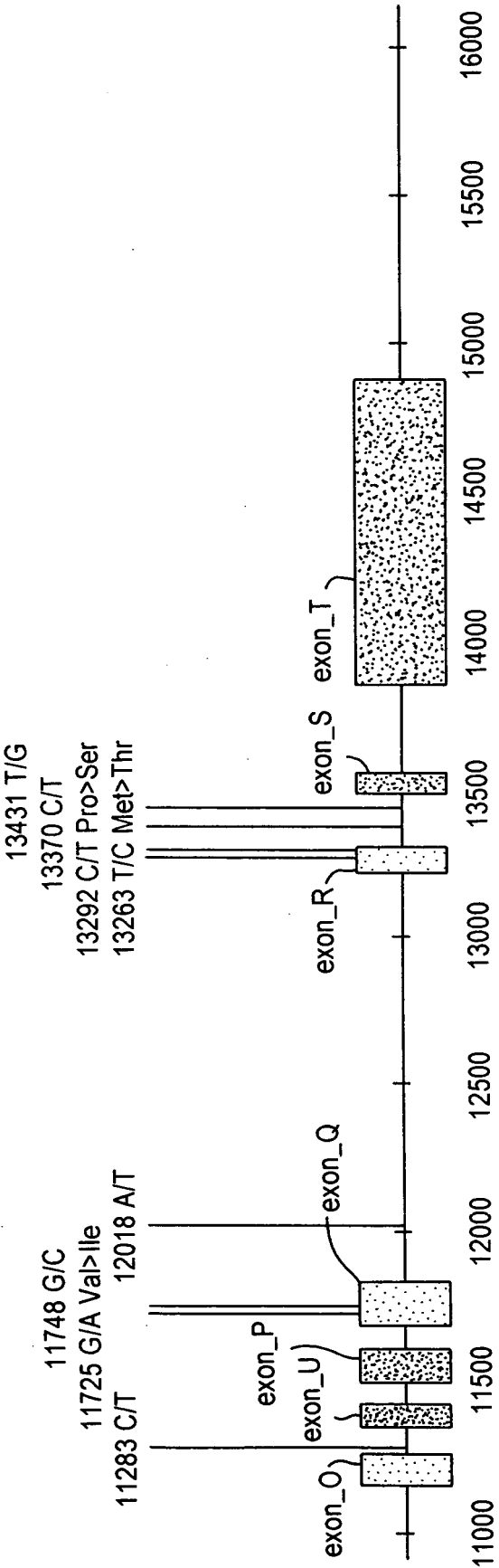


FIG. 15B

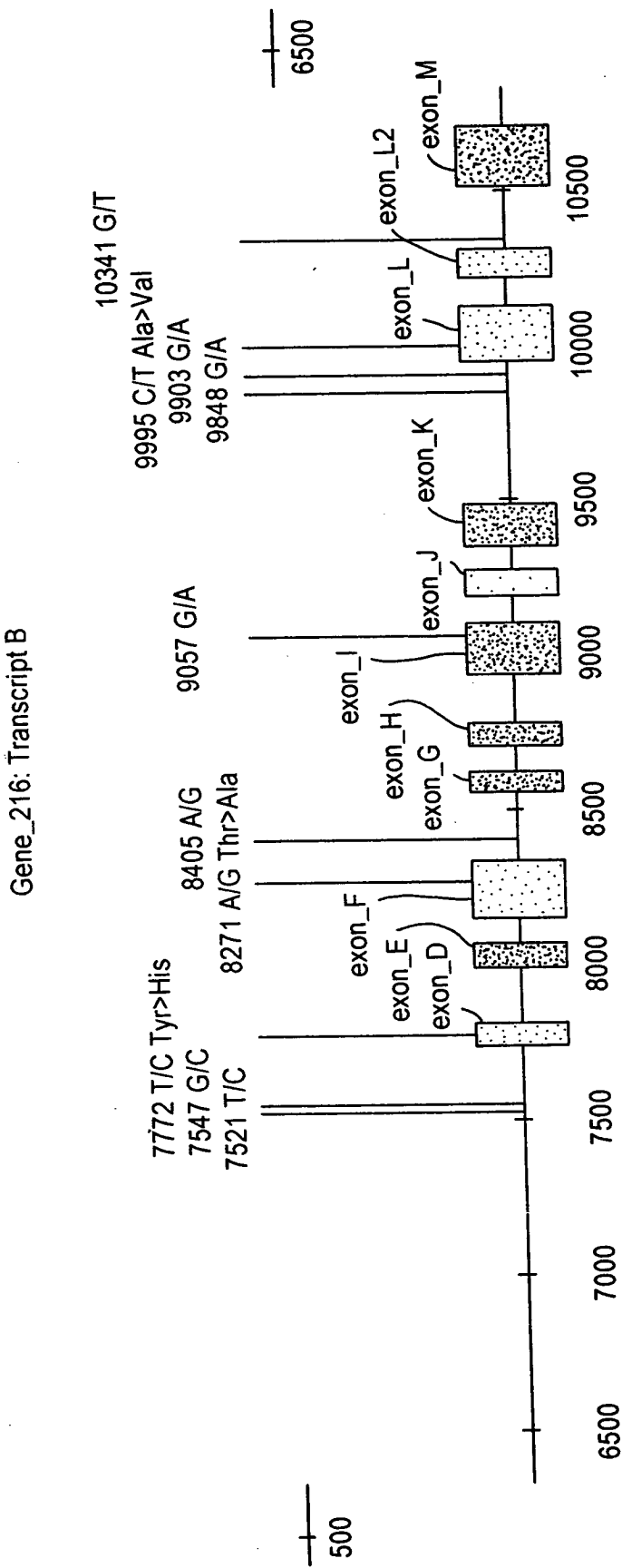


FIG. 16A

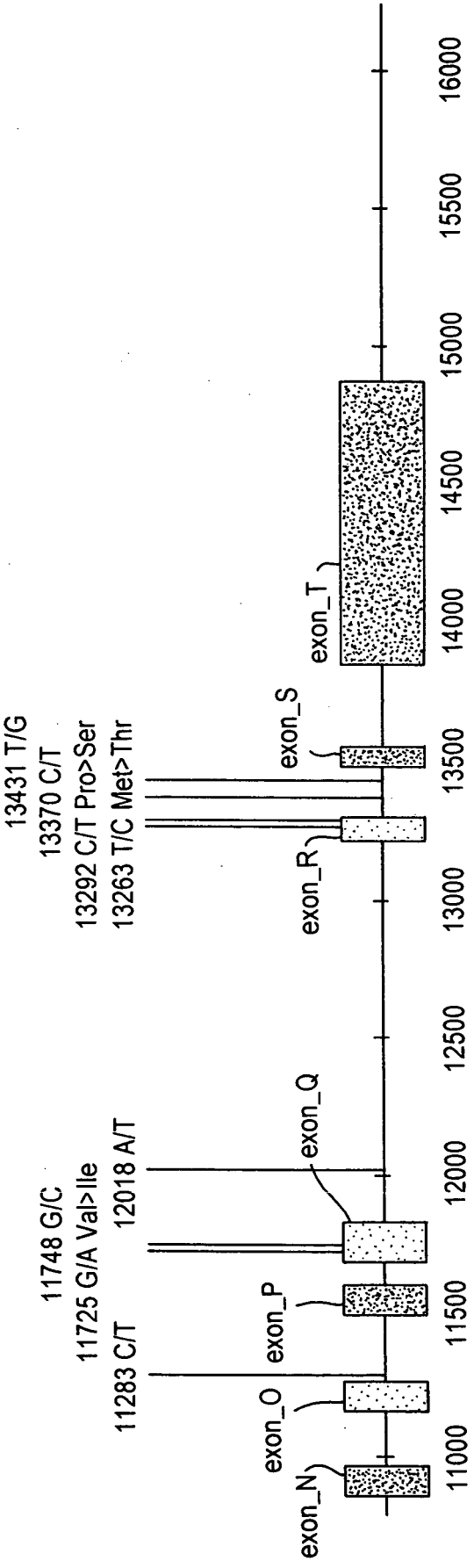


FIG. 16B

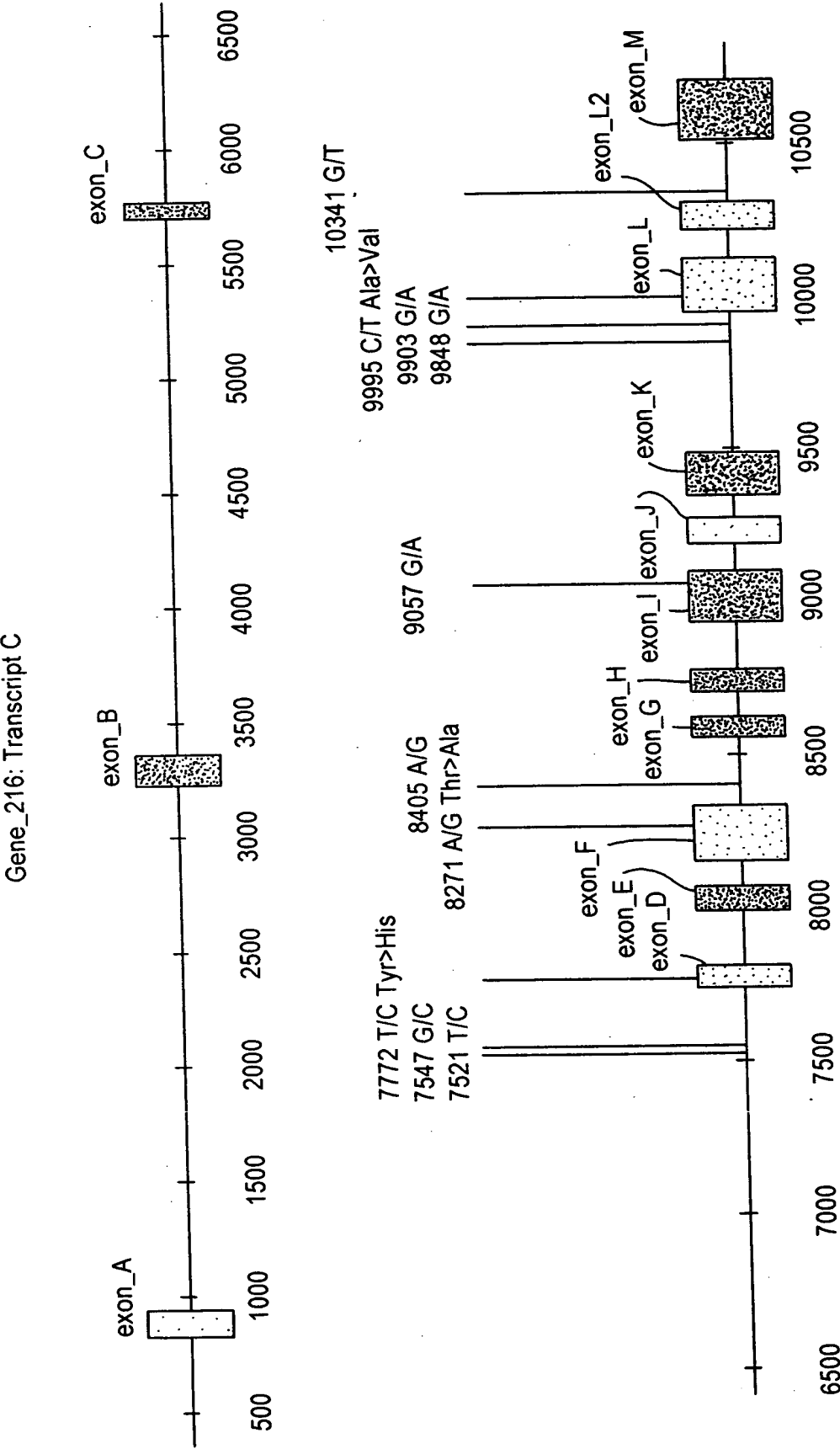


FIG. 17A

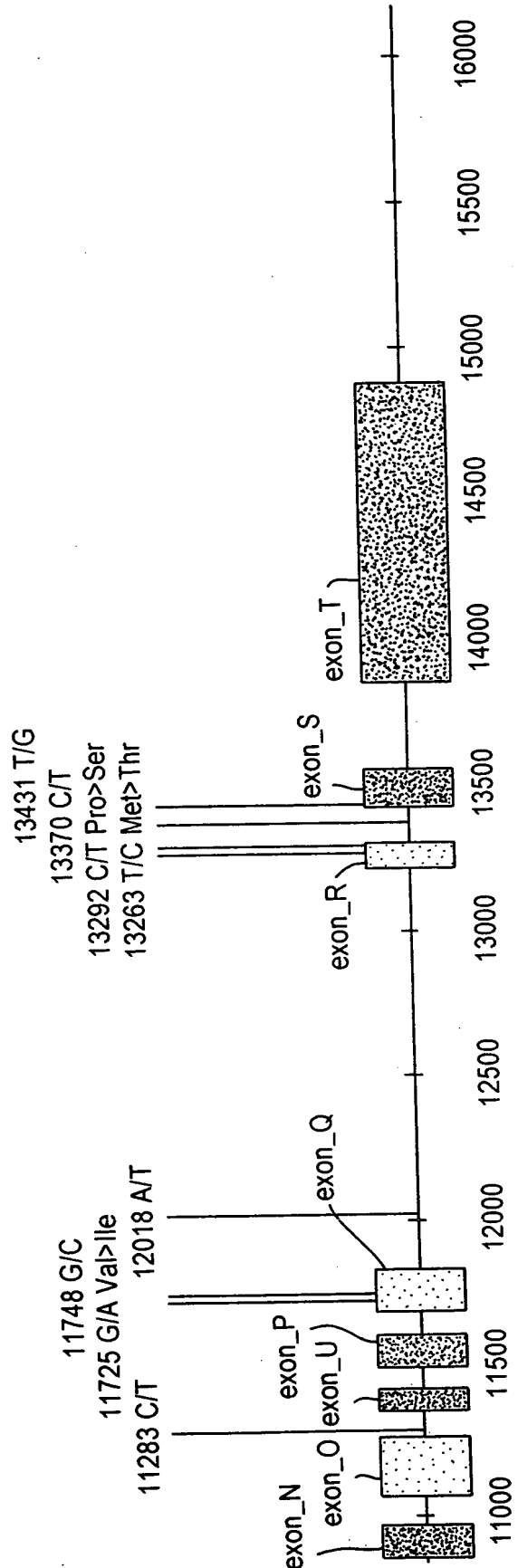


FIG. 17B

[illegible]

FIG. 18A

FIG. 18B

TCCTCCTGTCCCCAGATGTATTCTCACTCTGGTTTGCTTCTCCAGAGCCCTGCTCAGCCT
CCTCCTAACTTCTGCTCATTGTGTTCCCCCAGAAGAGCCATGTGTGCCCTTCACTGCTTCG
CTGCCCATGGGGAGGCCCGGCACTGATCCGCTGGCTTACAGAGAGGCAAGCGAGCCCCAC
AGAGCTTGTAAGTTGCTCATGCTTGAATAGTTTATTGGGCCCTAGAAACCTGAGGCTCCG
TGGGACCTAAGGGCTTCAGATGATTGGCTGCCCTCCCCTTCTTTCTATACTACTCAGGC
TGGAGAGAGTTCAATTCTGTACCTCCTGACAGAGGGCAGCCCCACTGTCCAAACCTAGAG
TGTTGCAACAGTGAGGATGCATTCCCAGAAACCTAAACCTTCCAAGTCAGGGCCTTCACT
GGGGTCCCCCAGACTTCTAGGACTTCTCTCAACCAAGCAAAGATGGCTTGTGGACATGCA
CGGGTTCCTTGATGGTGGCCTCTCTCCTTGCCCTGGCTCGGTCTGTGAGAGAATCCCAGG
GGGACTCTGCTCTGCGTTAGGAAGCCTGTGAGGCCAGGCCAGGAAGAGCTTTGGCAGGGT
GTGTGTATTTACAAACAGGGTTGTACTGCAGGATGGGGATGGTGCACAAAGGGGGAGGG
AGACCTTGGAGCAGAAGTAAAGGCAGCAAGGGCCGAGAGGGAAGGGACCTTCCACTGGG
GCTACTGCCTTTCTCCAGAGCAGACATTTTCCATAAAGCAAGAGGCACCTCCAACCTATA
TAAGCTCATGTTTGGGCCCTTGTGGAGCCTGTGGCTGGGGAAAGTGAGGGCCATCTTCTCT
ACACCTGCTGCAGAAGGGCCCTGAAAGATTCTTGGCCAGGGTCCCAGCCCAGTGCATTTT
GGGATAAAAAGGGAAAGCCATCGTGGGTGGGGAAAACATTTAAAAAAAATAACAGCAGC
CTCCCCTGGAATCTCTTGGGCTAGTTCCAGTTCTGGCTTCTAGCCAGGCTAAGTGGACTA
GCCTGAGAGAGACCAAGTCAGTGAGAGAGGAGAGGTGGCTAGAGGGCCAAGGCCAGCCCT
TCTGACATCTAGCTAAGAGAGTCAACACTTTTTAGGGAGCCAAAGTTGGGTTTCACTGTTT
ACTTCATGAGTTTCAAGTTATGAGGCCAGCTCAGAGGAATTTTCAAGGATCGGGCAGTTTGT
CAGAACTGAAGGTGGAGGAAAAGTTTGGGTTCTCTCAGGAATGAGGGAAAGGCAGCAAG
ATGGAGAGATGTGCAACCAGGAGCTGTGGATGCAGCTGGGTGATTTGGTGTCTGCTTGGC
ATGTGCAAGGCCCTGGGTTTGATCTATAGCACCCACAGCAAACTAGCAAGCAAGCAAAACA
AGCATACAAACAAAACAGAAGCAAGGTTGAGGTTAGTACAAGAGATGGCCAAAGCTGTAG
CCCACCCAATGACCCACATCACCTCAGTGCCCACTGCCTCCTGCTTTTCTGCCTTTTC
ATGGGGCTCCTGACTATGGCCATAGCATATGTCCATAGCAGACATAACAACATATGCCAG
GCAACGTAGCAACTGCTATGTCCGTATATGGTGGTTATGCATCTTTAAGGGTCCGTTGTC
ACAAACACAAGCACTGAGAACATCTCTAAGTTACAACCTCCACACATATCCACTCCCTGC
AATGCGAGAGCCAGCTGTTTCTATGAGCTTTCTCACTAGGCAGCTCTACATCCTACCGGT
TCTTGGGCAGCCAGGTGGCCTTGGGGCCTAGTGTGTCACTGCGTTTCTTCTCGGTGAGAT
CTTGAAGCCTGACTCGGTGCTGGTGGCTTTAGAGGCTGAAGGCCAGGATCTCCTGCTTGA
ACTGGAGAAGAAGCAGTGAGTACCAGCGGGGGGGTGGTGAAGTCCAGACAAAGACCCTC
TCTGGAGAGGATCAGTGCTTTCTGGGAGGGGGTGGGGGGTGGGTGGGAAGCAGCAGTGG
GAGTGACAGGGAGAGTGGCGGATGTACTTGGGGCTACAGTGGACTGAACCCAACTGTAGG
AAGTACATACCTGGTCATCTCATACCCTGGAGCAGCTGGATGGGCGGCTCCCCGCTGGAG
AAGAGTGAGCACCAGAACAGACATTGACTGATACCTTAATTCAAAGGGAATTCTTAGGCA
AAGGGAACCTCCACAGATGGCAGAAGAAAAGCTGCGAAGGTCAAATCCAATGGTGACAG
TTCATCTGGTCTACCTGGAATGCCTCCATCTGCGTGGAAGAGAACAGAGACATCTGGTCT
ACCTGGAATGCCTCCATCTGCGTGGAAGGGAACAGAGAGGAGAGGGCTGGGGTGGGGGGC
TTCCAGTGGGGCCGATCGAAGAGGGCATCTTAGTGCTAAAGATCTTGGATGGACCTAAA
GAGTCAAAGAACGGGAGGTGGTAAAGGAGAAACACAGTGTGGAAGGAGTGCAGAGGGTAA
GCAAGATGGAGGCGTGGAACTGCAGACTCCACCACCAACCACCACTCGCTCATGTCTG
CTTTCTTACGGACATTGCGAAGGCACTCATTCAATTTATTCTCTCCATGGAATCAGACA
GACTGGGAACAACTGCAACACCACGCCAAACCACAGTTCTGACAGTGCCACATCCCT
TCCTACTAAACGGTCTTGTACATGTGTGCACACATTGAACGTTAGCATGTATGAGTGCAG
CCAGCAAAGCAGCAGAGTTGTAATGTGTGTAAGGATGGCTGGCCGTACAACAGCCTGGGT
TTTTGATGGAGACAATGTGAATTTGGAGTCAGGATTTTCTGTAAGGAAGAGCAATTGAA
GTCAGGCATGGAGGTAGAGGCCTGTAAGTCCGGCTCCTCTGGGCAGGAGAACACAGAGTC
AAGTCAGGCACTGCCTGAGTTATAAAGAATGAGTTCAAGACCAGCCTAGGCAACTTAGCA
AAATCCAGTCTCAAAATATAAAGGAGTGAGGAAGAGGGAAAGAGAAAAAGAGGAAGG
AGAAGGAGGAAAAGAAAAGAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG
GAAGGAAGATAAAGAAAGAGAGAGAGACAGACAGACAGAAAGAAAAGACAGAAGACAGAAA
GAAAGACAGAAAGAAAGAAAGAAAGGAGCAAAAAGCAGCTATTTATTTATGGTTGCAATGT
TCCTGGTGGGGACAGGGAAGAGCCTGAAAATGGAAACATTACTGATAGAGTCTAGCTCC
AGGTAAAGGGACCCTTCCCCGGGTGGCTGAACAGAAGCAGCTACAGGCAGGTGGAAGTCG
GAAGTACGCATCACTGAGGGACAGATGGAGACATGAGATCTAGCAGTCTGAGGAGAACTG
GAGGGCCTGGGGTCCGCTCAGCAAAGGCAGGAGTACCCTGGCCCTACTTGGCCTCTCTGA

FIG. 18C

FIG. 18D

CTCAGAGGTGAGGTGTGATGCTGAGGGTCTGCAGCTGTAAAGTAGGGCGGAGCATGCCGA
GGGAACACTCCAAGTTGTTGACCACCTTCCACTTCCTCCCCAGGGACGCTCTGTGTGGGA
AACTGCTGTGCCAGGGAGGGGAGCCGAACCCACTAGTGCCGCACATAGTGACTATGGACT
CCACAATTCTCCTAGAGGGCCGCGAAGTGGTTTGCCGAGGGGCCCTTGTGCTCCCAGATA
GTCACCTGGACCAGCTTGACTTGGGTCTGGTAGAGCCAGGCACCGGCTGTGGACCTAGAA
TGGTGAGCCCTGCCACCCAACCCCTCCTGGTTATTGAGTCCTCCATGCCAAAGTGTCT
CCTCACTGCCCAGTGGGCACAATGCCCATAGGTGTGCCAGGACAGGCACTGTGAGAATGC
TACCTCCCAGGAGCTGGAACGTTGCTTGACTGCCTGCCATAACGGTGGGGTGAGTAGCCT
AAGGGGTCAGGGTGACCTTGGAGGTCCTTGCTACCTGGTGACTTTTCTATCCTCATCTTA
GGTTTGCAATAGCAATCGTAACTGTCACTGTGCTGCTGGCTGGGCTCCACCCTTCTGTGA
CAAGCCTGGCTTGGGTGGTAGCGTGGATAGTGGCCCTGCACAGTCTGCAAGTATCCCAAT
GGGGTGGGGGCAGGCAGGAACCACTGGGCAGTAGCCTGCTTGAGACTCAGCACCCCTGC
CCTCCACAGACCAGATGCCTTCCCTTGGCCATGCTCCTCAGCTTCCTGCTGCCTCTGC
TCCCTTGGGCTTGCCTAGCCTGGTGCTACTACCAGCTCCCAACATTCTTGTCTCGAAGG
GACTGTGCTGCAGGAGGGACCCCTATGGAATAGGTAGGTTCCGGTGCTCAGGTCTCTCTT
CCTGAGCCTGCCCCATGGCTCCTGCTTCTCAGAACTCTTCAGGGCTTTGTAGAGTGAGA
GGCTACAGGGAGCTGGGGCTTTAGGAAGCTAGATGGGATCCTTATTCTCTAGATGTAGTG
AGAGCTCCAGGCTGTGGGAAGAAGTCCGTGGTGTGTATCACTGCCCTGACCAGCACTTG
GTGGTGTGGTCCTTTCCATGGGCTTCCCTTGATTTTTTTGTTTTATGTTTTTTGTTGTTG
TTGGTTTTTTCTGCTTTAAAGAAATCAACACAGCCTGTGCTCCGCTTTGTCTGAAGA
CGACTCTAGCTTCTTGTCTCAATATCAGCCATCTCCCATGGCCTTTGCCCTAATTACTC
CCTTCAGGTCCCTCGGTGCTAGCCAAGGACCCCTTTGTGCTCCCTATAAACTGGCCAGCT
ATAGTGTGCTCTTTCTGTGCCAGGACTCTGTGCCTCTGTCCCCTGTAGATCACAGTGCT
GTAAACCAATTTCTGGCAGGCAGAAATGCCACCTGATAGCACACATTATCTACCGAGG
GCAGCCTCCTCACTAGGCCCCCTCGGGCAAGTCAGGCACATTATGTCCCTGTCTGAACCTG
GAAGTGTCTAGACCAATTGAGGGAAGGGCAGGGTTGGGTTGGAGATGTGACTAGAGGGC
ACCTCAGGCCAGAAACAGCACCAGCAGGCCCCAGGAGCCAGTGAGACGGTCTGGGGAAAG
CCAGGTAGTGCTGGGGGTGGGGGCGGTGTCTGCAGACAGGAAACAGGTGGAGTGACA
GTTGGGAGGGGGCACTTCAGAGGGGTGGCAGCTGCACACCGTTATCGGGATAGGGTGTC
AGGACAGTGGGAATATCTGGATGAACCATCCAAAGAAATGGCAAGGTCTGTGAGAAAGGT
CCCCGCCAGTTCAGAGTCTAGACTGGCAGAGCAGGCTAAACGGAGCATGGGAAGGCACAG
TTCCCCCAAGGGAGACATCTCTGCACTTCAGCTCTAGGTGGGGCCCTCGGTGACGCCCTAC
ATCTAGACTGAGTGGGGGCTGGAGTGGAGTCACCTCGGGAGAAAGGATGTCCACAGCCCT
GGAGGCCCTGGGACATAAGTGAGGTCTGGACATCTTAAGGACAGAACAGGAATGTGGAAT
TCGAAGCTTGAGTGGAATGGAGAAGCAATCCCCCTTTGTCTCATACACGGTCACTTTCCA
ACCTTCTGAACCTTTATCTGGTCTGTCACTGGCCCCCTGCAGAGACATACCCCTGGGCAGT
GTGCATCCGGTGGAGTTTGGCTCCATCATCACTGGAGAGCCCTCGCCCCCTCGTAAGTGT
GCCCCCTTGGGACATGGAGAGGGAAGCAAGGGGTGGGTGCTTGCCATCTGCCTCCTTCTAA
ATGCTCTCCTTAACACACCTTCAATCCTCTGCCCTGCTCAGCCCCATGGACCTCTTGCCA
ACAGCGTTTCGACCCCTCCATCTCTTGACTTGCTCTCAGACCCTGCGAACTCTGAGCTTAC
CTAAGAACTACCCCTCTGAAGCAGCCTGGTCTACAGATTGAGTTCAGACCTGCCCTATCC
CTATGGTATGGAAGCACCCCTGAGGACCTCCTGTTGCCAGTCACCTACCTCTGTCTCAGT
TTGTTGTCCCTCCTCAGATTTACAGGCTTGCAATCAATAAAGAAATGAGACATGGGCCTC
AGAGAAGCTGTTGTATAGAGACCATGATGCTGGAAGCCCTAGGGGCAGGGAAGGGAGAC
ACTGTGGTCTCTTCTGGGTCTTATAGAGGGAGGACAAATGTGCCCTGCCATGTGACTTG
CAGTCCTCAGTTTCTCAGACGCACTCTTATAATTCTATGGGCTGTATGCTGAGCTCTTA
CTCAGCATAGGAACCCCAAGAGCCGATCATGTTGTATCCCGCTGCCCTGAGAGCTGTGC
TATTCTGAAATGTTAGAATGTATCTAATAACAATAAATCCACAAGTTATATCAGTGTTGT
TGGCTGTGACCTGTAAAAGGGTCTAAGTTGTTTATTAAGAAAGATATGGAGATGGATTAC
TGAGAAAGAAATAGAAACAACATCTGGACAGTGGAGGAGCCAGCACTGGGGAGGAAAGG
GCAGACAGATCTCTGAGTTCAAGGCCAGCCTGGTCTACAGATTGAGTTCAGGATAGCTA
GGGCCACACAGAGGAAACCCCTGTTTTGAAAACCAACAGTCAAATAATAAAACAAACTT
AGTAGCACCTTGACAGACAGAGAGAAAGGTTCCAGGAGAGCTCAGACCCAGCACCAG
AGGTGGCAAGGCAGAGTCTCAAAGCCAGGTGGGAAAAGTGGGATCTGTTAGCATAAACC
CAAAGGGCGCGTGGGACAGGCAGGGAGTACCCTTTGATGCAAGCTCACTCTGGTGAGGGC
CCCTCACCCCTGGATGTCTGTTAGCAAGGGAATCAGTCAGTGTCTCAGTCTGTTAACATC
TGTGAGAGGGGAAAGGCTGCTGCAGACATGGCCTGAGCAGCATCTGGATTGGAACATTTG

FIG. 18E

CACTTTAGGGCCTGCTCTCTCCCCTGGGTGGGGCACTCGCCATTTCATTGCCTTTACGACA
 GCTGTGAGAGAGAGGTTGCTGCAAGTGTGTATGGCTGGGTTAGCTCGAGCCCACCAGGCA
 ATCATGATTTCCCTCGACATCTAGTCATTAACAAACACAGGTTCTTTTACTACAATTTTA
 ACTACCAATATTAACATAAATGTGTATAAAATATATAACACAGTACACATATATAAGTA
 CATAGATGTTAGTACATATAAATATTATATATATATATAAATTGTAATTAATATTACTT
 AATTTTATTTTATCATTGATATTATTTTACTGTAGTTATAACAATGTGCATAATATAT
 GTGTAATATAAAATATAATTTTATTATTTAATATTATTATATAAAATTTAATTAATATTAA
 TTATACCTATATATTTAGTACATATACATAGGTTACAGAATGGCTACAAAAGTGCCAGGA
 GCCATCAAGGAGAAGCTAAAAGCCAGCAAGTGATCTTCTGAGACGGTTCTGCCATGGAC
 TGTACAATTAGTGATGGATTGCTTCTGTAGGCAAGGACGAGGAGATTTCAATTTAGGAA
 AGATTCTGCTATTAATATGCTTTTCTGGTATTATTAAATATATATAACAATCACTAGG
 TATTAGCCACCGTTTGAACAGAAATGTTCTGCAGAACAAATGAAGATGTACTCTCTTGTA
 ATGATGCTATATAGACAAATAGATTATTTCTTTTTTAAAAAAGAAAAAGAGCCGGGCGA
 TGGTGGCACATGCCTTTAATCCCAGCACTGGGAGGCAGAGGCAGGCAGATTCTGAGTT
 CAAGGCCAGCCTGGACTACAGAGTGAGTTCCAGGACAGCCAGGGCTACTCAGAGAACTC
 TGTCTTGGAAGAAAAAGAGGAAGAAAGAAAAAGATTTATTTATTTATTTATACAT
 ATGAGTACACCATCAGACACACAAGAAGAGGGCACCAGACCCCATACAGATGGTTGTGA
 GCCACCATGTGGTTGCTGGGAATTGAAGTCTGAGACCTCTGGAAGAACAGTTGGTGCTCTT
 AACCCCTGAGCCATCTCTCCAGCCCAATAGATGATTTCTTAATTCTTAAGGATGATCCT
 ATAAGAATTCCTAACTTACATTAGTAATTATTAAGCTCTTTTACAATAGGACTTCTATT
 AAGTCTTCTCTAATATGAAAACCTCAATAAGAACTCTGCCAGTCTCAAGTGTCTAGT
 TAGTTGCTTCTGAGATAGCAAGTAGGCATCAACAACCTAGAGCACATTCTAGGAGGTTGT
 AAAACCATTAAACAGTGGTCTTAAAAAGGGAACATAACAATAGGCTATAGGTGCAAGGACA
 GAAGATAAAATATTGACTAGGTTTATCAATACAAAATTTACCCACAAAAGTTATGTTTTT
 GACTTTTTCATAAAAACCTCTTTATGAACCTGTAGAAGTGGTGAAAGATGACGAATGCTTAG
 CCAGATAATTACTCCTAATAGATATGCATGTGAATATTCTGTGCTGTAAACTTATTTATG
 TTTGAACCTCCAGTGAACCTTTTGTTTAAAAAGGGGGGGGGTTGAAAAGCCATGTGATC
 TATTCTCCTAGAAAGGGTACAGAAGACTAAGAAAGATTACATTGGAGATGTAACCTTGGGA
 GAGAAAGCTTTGGGAGCAAGAGCATAGAGAGCAAGGCCATTGTGGCATCAGAGCAGGAGG
 AGAGAGCAAGATTAGAAGGAGATGCAGAGTGGAACTAGAACTATAAGGCAACATA
 AAAAATTAAGAGAGCCATATGCAGAATGCAGAGGGAAAGAGAAAAAAGAAAAAAGA
 AGCTGCAGGGAGAGCAGAAGGAGCAGGCAGGCTTCTCCTGACCATGGGGTAGAACAGGGC
 TTTTCTTAATACCAAGGCAGGCTTAGTCTTAAGGATAATAAAGCTTTTCTTTCTTACAGA
 CTTGGTTTTAATTCATTTAGCAATAAAAGTGTAAGAGTGTCTTTTCCCTATGCAATAA
 AGATTGGAGCTTATTTTTCAGCCAGAATGAGTGAGTTCTCTCTGCAACGGTCTTGGTCT
 TTTGCTTACATATACACACATAAGTGTGTGTGTGTGCGCGCATGCGTGTGTGTGTGTGT
 GTGTGTGTGTGTGAAGTGTGCAATTATCAGATGGCATGGAAGCTGGGCTCAATTGGTTC
 AAATGGGGACTTGTGAGGGTATATGCATGAATCTGTATATGAATTCATGTGAGCTTATAT
 ATATTGCTTGTGTAAAAGTTTTCTTCTGTGTGAGTGTGACTCTCTTCTCCTGGTTCAAT
 AGAGGTTTATTGCTTCAAACCTTCCCCCTAGCCTGACAGTGCAGAGGCATCTGGACAAGAG
 AGAAAAGGCTCTAGCCATTAATCCTTTTCTTAGATCCATTTTCTTAGAGAÀCTTTCTTAG
 GAACTGTTTAGAGAGAACATAGAAAACAGGCTGAAATCACTTGTCAACTGTCCCCTTTT
 CTTCTTAAGGACTTCTACTAGCAGACTGGGAGTTAGAGCTGCACAGTCCCTGAGGAGATA
 GAACAAAGGCTGCTTTACTGAATCCCCCTGCTGTTTTAAGATGAGGTTCTAAAGGAGATTG
 CAGTTTCTGACCCCCAAAAGGAACTCAGGCAGGTCAGCTACAGTATCAAAGTGACTTAAA
 CTTAAGATAGGGATATGTTTTATTATTAAACAGCTACCCTAAATATCTCATAAGATCAAG
 CTTACCCCGGTGACACTTCCCCCTCTGTTGCCTCAAGAGGAACCAAGCAGAAAGAACCGC
 CAGGGCTGGCTCCTGGCACAAATGGGTTAAAGATGTTGTAGCATGGGGAAATGAAGAGAT
 GGCTCAGCTATTAAGAGAATATCTTACTCTTCCAGAGGACCAGTGTTCAATTTCCAGCAA
 ACATATCAGGTGCCACACCATCACTTGTAGCTCCAGCTGCAGATCTGCTACATCTGGCCT
 CCATAGGCACCCACACACAGGTGGCACCACAAATTAATAAATAAGATAAATCTAAAACA
 GCAAAGTTAAAGCATGAGCTGAACTAGTAAAGTGCTTGTGTGGCATAGACCAAGACCTG
 GGTTTGGTCCCTACCTGTTAGAAATAGTCTCAGTATCACACAAAGGAACACCCAAGCGAA
 GCAAAGCTCCCAGCAAGACAAAACCTACAGTCTTCATTGAGAGTGTGCACGCTGAAGACC
 GAGCACACTGGGTGCAAAATGTACTTGGATTCTGTTTGTGTTTGTGTTTGTGTTCCAGACAGGGT
 TTCTCTGCATAACAGCCTTGGCTGTCCCTGAAATTCAGTGTGTAGACCAGGCTGGCCTCA
 AACCTCAGAGATCCGTTACCCACGCTTATCTAGGCTTCAGTCTCACCCTGTGAGATGG

FIG. 18F

CCTGAAAGTTGTTAGAACCGCGCGGGATCTATTTCTGACAGACTGGCTGGCATCTTTTCC
TTCTCTCAGCATGAGATTCTTGGGGCGTTCCCATTTTCTGACATCAAGCATGGTAGCAGAGT
TGGAACCTGAGGGCTGAGGGCTCAGACTCAGACCATAAACTGGAAGCAGAGAGAACTGGA
GATTGTGGGAGGCTTTGAAACCTCAGCTCCTGCCCCAGCAAATACCTTCCAGCAAGGCCA
CACCTCTTAAACCTCCCCAAACAGGGTCACCAACTGGGGACCTAATATTCAAATGCCAC
AAATATGGGAGACATGACATCCAAACCGCCAGGACAGGTGTATACCTCCATGCTTGGTTT
CCGTAGTAAGAAACACTAAACATTAGCCTTTTCTTAATAAACTGATATAAAGCCCTGCT
ATTCTCGATGTTTTTCTCTGTCTGCTCCTCTTCTCCACCTGCTTCTGTCTCTGA
CCTCTTCTGTGTACAGATAGCCCTGCCATGTCCATCTGCCAGCCATGTTCTGTCTACTT
GCCTCTCTCTGTCTGTGACTCTTCTAGATGCCTCTGGCTGTTCTTTCTCATATCTACA
ATAAAAACCTGGCCCTTAATCATACCACAGAGATATCGAGTCTTCTTTATACAAATTTTCT
TTGTAGCTCTCTTAAAGGGAGATTAAATAAACAGGCTGAGCACACAGGAGGATCATGGCA
TATTGACTTGCTTGTGAGGTTTCTGAGATGTTTCTGAGGCTCTTGAATGAAAGAGATCTT
CATAAAATTTCTATCATACAGACAACAGCTTAAAGACTTGCATGGGAAAATACTGGTGAGTA
GGCCATGTCCAGGTTACTAATAGCCTCTGCACAGGGAGAGCCCACTGTGGAGAATAGGC
CAAGGACAGGCCGATAATCGCCTTATTTAGATCTGTTCTTTAAGATGTGTGTGTGTGT
GT
AGCTGTCTTCTGACACACAGAAGAGGGGCATCACACCCCATACAGATGGTTGTGAGCCAC
CACATGGTTGCTGAGAATTGAACTCAGGACCTCTGGAAGAACAGTTAGCTCTTAACCAT
GTACCATCTCTTCTGAGCCCTTCTTATATTTGTATTTTAAATAGCTTAAAAAGAAAAAGA
AACCATGAATGTGAAATTAGCATAAACTTTAGTGTTCAGAAATAGATTTTTTTTGGAAC
ACAGCCAGGTTCTTTCTTGTGTTGACTGTGTGAGGGCATTCTGGGAAACAGGGTGTGGCC
TGGGAAGCTGTGAAGGTGTACTTCTAGTTCCTTCTGGCCCTCCTGCAGACAGTGCAAGCC
CCACAGTACACTGCTGCATGTCTGGGGAGGTTGTTCCAGCTGCTGAACAAGTTCTTGTGG
AACACTGTCACCCCTGCCCTGGGGTCATAATCATGACACTGCTGCTCCTCAATGTTTGAAG
GAAAAACACCCCTTAGTCTCAATGCTGTATAAATAAACCCCTCTATAAAATCAAAGGCCGC
ATTCCATAGGATGAAACACGCGGGGAACATTTTCTTCCATGCCAGGCCTTCTCTTCTCTG
GCAGGGCTCCAACATGTCTGGTCTGCCTGCCCTGACGCCAGGCTACGGCTGGCTGACTC
CTTATCAGGCACGTAGCCCTCCTTGGTCTGTTCTACCAGTCCCCAAGCCTAGTCCAG
GTCAATGCACAGATTGAGCCCTGTAATAGTAATCTTGGGGAGGGGGCGTTCTATGTCC
CTTTTTGCTCCCAAATAACTGCAGAGTGTCTTATACCCACTCGAGCCGTAAAGATACAG
AGACCTGGCATTTTTATTAACAAGCTATTAGAGTGTGTAATATCCGGGCAGATTC
TTATCTATCCTAACCCAATTAGACTACCTACTACCCAACCAATGCCCTGGTACTTGCCC
TCTGGTCTTGCCCTGCTTCACTCTGGTCTATGTATGTTCTCATGGCTGTTTTCTCATGGC
GAATCTTCTGGTCTCTCCACGTGGTTTTCTCCACACCGTCTCCTCCTCCTGGTCTTATC
TACTCTCTGGTCTCCTTTGGGACCCCATGACTGGGATTGGAAGTCCCTCCCTATCTCTC
TGCTCAGCTAATTGGCTGACCAGCTCTTTTATTAACCAATCAGAGGTGATGGAAAACAAT
GTTTACACAACATTGAGATCGGGAGATGGCTATCTTCCAGACTGCAACCAGATGTCTGCG
GTAAAGAAGTCAGCATCTGAACAACAGTGCACAAAACCATCCCCAACAGCCCACTCTG
GCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCT
GAGAGTTTGGTTTCCAGCAACCAGCCTTCCGAGAGCTGGTGGCCTTCTCTGGCCTCGGGG
TAACATGCATACATGCCCCATAAAATCTGCTTTACAATGCTGTCTTAATCTGACCAGAAG
AAAAATGTAAGACTAACTCAGTAGAAATAGTCCAGGAAATAACTAGTGAGAATTCTTATGA
AAAAATGGGGATAAGGTGAAGGAGAGTTTAAACATCCAGGGGAAGTTGGGACGGGCTTCT

FIG. 18G

>Mouse 216 homologue aa sequence

MGSRCGRPGGSPVLLLLPLLLPSCPLRSARMFPASIPKPHLHIPTCTWLTNYEAHVTLRT
RFELELLLFQILKMYMSVLPAAHASVYRGGNAHGEIVTPHWILEGRLWLKVTLEEPILKPDS
VLVALEAEGQDLLLELEKKKKLLAPGYTETHYRPDGHVVLSPNHTDHCQYHGRVRFRE
SWVVLSTCSGMSGLIVLSSKVSYYLQPRTPGDTKDFPTHEIFRMEQLFTWRGVQRDKNSQ
YKAGMASLPHVPQSRVRREARRSPRYLELYIVADHTLVSPSDSQDSGYTVGVDRAGSVDR
AGSQSHHSGRKRNALGFPTVAPRGVVGQETTRLHTTAHDHSELPIGTAATMAHEIGHSLGL
HHDPEGCCVQADAEQGGCVMEAATGHPFPRVFSACSRRLRTFFRKGGGPCLSNTPAPGL
LVLPSRCNGFLEAGEECDGSGQLKSAGTPCRPAATDCDLPEFCTGTSPYCPADVYLLD
GSPCAEGRGYCLDGWCPTLEQQCQQLWGP GSKPAPEPCFQQMNSMGNSQGNCGQDHKGSF
LPCAQRDALCGKLLCQGGEPNPLVPHIVTMDSTILLEGREVVCRAFLPD SHLDQLDLG
LVEPGTGCGPRMPHGPLAN SVRTLHLLTCSQTLRTLSPKKNYPLKQPLQIEFQTCPIPM
REDKCALPCDLQSSVSQTHSYNSYGLYAELLLSIGTPEPDHVVSRLP

FIG. 19

>Gene 216 genomic DNA sequence

CCAAAAGCGAACACACCCAGATCAAGAAATAGACCATCCTACAGTCCCCCCTTACACTCT
GTACCAGTTGTCAGCCCCCACAAGGGTAACTACTGTCTTGACTTCGAACACCATAGATTTG
ATTTGCCTGTTTTTAACTTTACATAAGTAGAATCACAGAGTGTGTACAATGACTTTGGA
AAACTGTTTGACAATATCTATTAAAGCTAAAATACCCTTGCCCTATGAACCTGAAATTCC
ACCCACCTTGCCAAGGGACAAAAAGTTCCCCTCTAAATGCACCAGGCTGTCAGGGATGAA
GCGTTGGCTTTGGGGCCCCCATTACACACATGACCTTTTCTGGGGCACCCAAGCATCAG
CCTGTCGTCAACAGGTGCCACCCTGGCGATCTCTGAAGGCTGGAGTCGGAGTGCCTCCCT
CAGACATCCTGTTCTGCGTCACTCCTTGGGAGAAGTCGTGTTTACAGATGGTGGGTGTCA
CCCATGCCAAGCACTTCTAAGGGTTAATGCTCACTGGTTTGCCTGGTTCCCAGGACATTT
CCTGATGCCCCCTCTGGAGGGTGACGCCAACAAAGCCAGTGGAGAAGCCATCTTTCCCAGGT
GCTGTCAGGCGCCCCCGGAGCTGCTCGGTGCATCCTAGGATCCCTCTTCTCAGCTTTTG
TTTGATGGCCTCATCTCCTCCCCTGCAACCTCAAATGTAAATAAACCCCTTTCTCAGAGA
CTTCGGCAGAAAATTCCTCTGACCTGCACCTTGGACACAGCTCATCTGGGTTTGGGAGGTG
TCAACTGTGTAAAGTAGTACTCTGATCCCCATGTGGCTTTTCTGACTGTGTCCCCTCTACAG
TCAGTTATTAGCACTGACTGTGCTAGGAAGTGAGCAACACACATATTCCAGACCACATG
GAGCTCAGGAGCTTGGGGAGAGAGACAGGGAAGTGGACGACTACAGGGCCTTCTGAAACG
TGTTGCAGGGAGAAGTGTGAGTCAGTCAGGGGATGCTAACCTGGCTTTGGGTAAGGGACAGCCT
CTGAATGACAGGACATTAAAGCCATGGCCTGCAGTTTAAAGTAGGAGTTGGCCAGTTTCGAG
GTAAGAATAACAGTAAGCAAGAACGCCAGAGTAGCTCCTCGAGCTGCCTTCTGTACCTGA
CATCCACACTGAAGCCAGCCCCCTCTGTGTTTCAGCCTTGCTTTACTGAAGAGGTGTGCTG
AGGGGCTGCTCTGGGGTGCTGCTCTGCTTTCTGTCCCCAACTTGTTCTGAGCTCGAGCC
ACCTCCATACTGGTGCTCCTGGTTCTCAGGCCTTTGAACTCAAACCTGAATCACACCCTG
GCTTTCCTCGTTCTCCAGCTTGCAAGATGGCAGATTTCGGGAACTTTTTGGCCTCCATAATC
ACGTGAGCCAATTGCTATAATAAATATCTCTCCTCTTTCTTCTCTCTCTCTCTCTCTG
TGCAAATATAGTTCCAATTATAAGAGCCCCCTAACTGGAAAATAACCCCTATGGTGCACTGG
TGAGTAGAGAAACTGTGGTTCCCTCAAACCACCGAACACTATTCAGCAATACGAAGGAAC
AAACTATTGATATGCAAAATAGTGTAAATGAATCTCAAAAACATCGGAAGAGGGGAAGGA
AGCCAGACACAGAAGAGTGCATGCCGCATGATTCCATTTATATGAAATTCTAGAACAGGC
AAAACCTTATCTATAGACAGAGAACAACAGATCAGTGGCTGTCTGGGGTTGGGAGTGGGGA
AGTTTGGCTGGAAGGGCACAGGGCTCTTTCTGTGAGTGAGGGAATGTGTCTGCATTATAG
TGATGCTTATGTAGTTATATACACTTATCGAAACTCATCTTACTGGCCACTTAAAATAAG
TGCATTTTATTGTGTGTAAATTATACCTTAATGAAGTTGATTTGAAAATCCAAAGTAGTA
ATAATAAGTAATAATCTCGTAGCTGGACAGCTGTGGTGACTCACTCCTGTAATTCCAGCG
ATTTGAGAAGCTGAGGCAGGAGGATCACTTAAGATCAGGAGTTCTTTTTATTTTTATTTT
TATTTTTTTGAGACGGAGTTTCGCTCTTGTTGCCAGGCTGGAGTGCAATGGCATGATCTC
GGCTCGCTGCAACCTCCACCTTCTGAGTTCAACGATTTTCTGCTCAGCCTCCCAAGT
AGCTGGAACTACAGGCGCTCACCACCTGACCGGCTAATTTTTGTATTTTTTAGTAGAGAT
GGGTTTTACCATGTTGGCCAGACTGGTCTTGAACCTCCTGACCTCCAGTGATCTGCCCCG
CTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGACACTGCGCCTGGCCAAGACCAGG
AGTTTGAGACCAGCCTGGGAAACAAAGTGAGACCCCTGTCTACAGAAAAATTAAAAATT
TTAGCTGGGCCTGGTGCCGTGTGCCTGTAGTTCCAGCTACTCAGGAGGCTGAGGTGGGAG
GATACCTTGAGCCCAGGATTTCAAGGCTGCAATGAGGCATGATCAGGCCACTGTCCTCTA
GCGTGGGTGACAGAGTGAGACCCTGTCTCTAAATAATAATCATAAGAACAAACAGGACCC
TCTAAACGCACTGATATCTAAGGTGTATTAAGCGACCAAAAAAAAAAAGAAAATCAAAGT
GCAGAAAAACGTTAATAAGAGAAAAAATATGTCTGTATTGTCTTGAGTGTGAAAAATA
ATCTAAAAGCCTATGAAAGAACTAATCATATTGGTTTCTGTTGGTGAGGAGGGCTAAG
AGCACGGAGACTTTTCCCTATGCTTTCTGTACTTTTTGATTTTGAGATATGTGAATGTAG
GTTTCTCTCACTGCTCGAACTTTCACTAACCAAATTACTACATTCCAAATTCTCAAAAAC
AATAGATTTACTTAAAAGTAGGCTGGGTGCGGTGTCTCACGCCTGTAAATTCAGCGCTT
TGGGAGGCCGAGGCGGCAGATCACCTGAGGTGCGGAGTTTCGAGACCAGCCTGACCAACA
TGGAGAAACCCCATCTCTACTAAAAATACAAATTAGCCAGGCGTGGTGGCGAATGCCTG

FIG. 20A

TAATGCCAGCTACTCGGGAGGCTGAGGCAGAAGAATCACTTGAATCTGGGAGGCAGAGGT
TGCACTGAGCCCAGATCATGCCATTGCACTCCAGTCTGGGTAAACAAGAGAGAACTCTGT
CTCAAAAAAAAAAAAAAAAAAAGATTTGCTTAAAAGTTAACATCTCCGGCCGGGCGCG
GTGGCTCATGCCTGTAATCCAGCGCTTTGAGAGGCCGAGGCGGGTGGATCACGAGATCA
GGAGATTGAGACCATCCTGGCCAAAATGGTGAACCTCGTCTCTGCTAAAAATACAAAAG
TTAGCTGGGGTGGTAGCGCGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAG
AATCGCTTGAACCAGGGAGTTCGGAGGTTGCACTGAGCCAAGATCGCGCCGCTGCACTCCA
GCCTGGCGACAGAGGGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAGTTAACATCTC
ATCCAAATTTGCACCGAGTAGGAAAACAAAAGTTTAAAACATGAAACAGATGTTACTGAG
GCCGAAAGGGTCTCCCAGGCCTGGGAGTCTGCAGCTTTTATGCAATTCTGCCCTCTGGCC
ACCGCCAGGGAAGAAAGGTTGTCTCCGTCTGCTGCATCGCCTTTGCCCAGCAATGAAGCC
CCCAAGACAGCGGCAGCCGTTGCCTGAACCTTCTATCCTTGGGGGCACCCAGTGCAGG
TGGATGACCCGATCAACCTCCGCCAGGCAACCTCGGGGCAGGACGGGTAGCAAGGAGG
GGACAGAGATCGGCCCCAGGAGACCAGGAAGATCGCGCTCCTGGGGCCAACCTCAGCAG
CGAGAGGCGGCCTTTGCCACCGCCTCATCCACCACGCGCGGTCTCCAAGAACCTTC
CCAGCGGTTCTCTCCTCCTCTCAGGAGTAGAGGCCCTCTGAGACCGACGGGGAGGGACGG
CTCGGGCCGGTTCATCCGAGGGGCGCACGGATTCCCTCCTCCGCCAGCTCCACCCCTC
GAGGGGCGGCGGTCCGGGAGTGGCGACCCGGCTCCCCATGCGCGCGCGCTCGGGGCC
CTGGCCAGGCTCCGAGCGGGTGGCGGGGAGGGGAGGCGGGAGCGAGGGCGGGCGGTGG
GAGGTGGGGGCGGGAAGGTCCGAAGGCGGCGCCTGAGGCTGCACCGGGCACGGGTCCGC
CGCAATCCAGCCTGGGCGGAGCCGGAGTTGCGAGCCGCTGCCTAGAGGCCGAGGAGCTCA
CAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTACTAC
TGCTGCTGCTCTGGCCAGTGCCAGGCGCGGTGGTGGTGGCGGGGATGGGTTCTGCTCAGAGC
TCCGCCCTGAGGGGCAGGCTAGGCGCGGTGGTGGTGGCGGGGATGGGTTCTGCTCAGAGC
TGCGGCTCAGCGCGGAGGGTCTCACGGCCCCGGCACCATACGGCCAGTAGGTACGGGCG
TGGGGAATCTTTGGGGGGGTCTCCGTGGGACCTGCCAGGGACGCTCAAGTGTGCTTGGG
CTGGCCCCGGGCCCGGACTTGCCACACTGCCCGGTGCCACTCCGCTGGCAAAGCAGAG
GGCATGGCTCCCTCCCCCTCGGGGACAGCCAGCCCCAGCCCCAGCCCATAGCCGTAG
CCCCCTCTGCCTGGATTCTCGCTCTACAACCAGCTTCCATCCGCAGGCCACCGTGTGAC
CCGCTCCTGCTCCTCCACCCCTTAGGACTCAGCGGGGCTCCATCCTCTAGGAAGCCCCCA
TGCCCAAGAGTCCCCCAGAGTCCCTGCTTTGCTCTCAGGCTGCAGAACTAGCTGTGGCCT
CCACCCCTGCTCACCCCTCGTCCCTCCTCCAGGGCAGCAGGGCAGTGTGTATGTTGTTA
TATTGTTGCCTTGTGTTGGTGAAGATAGAGAAGGGCCTCTCCAGATAGAAGGTGTCTGTTA
GCAGTGCTCTGGAAGACTGCAGCTGTCTCCTCGGGGTAAACCCCTCCAAACAAAGATGTT
AAGATGGGGCTGGAACAACCTCTGCAAGCGGGTGGGAGGATTAGCCAGTCTGTCACAGCA
AGTGCCCTGGCCGGAACAGGGAGGGCAACCAGGGAGGGGGCATGCGGGGCTGGGCTGTGC
TATGCAGACTGGGCGGTGGCTTCCACAGCACTGTGTGGGGACCAACAGGTACAGGGGCC
TGGTCTGTTCTGGCCCCAGGGGAGGGCCCCAGGCGGTCCACTGCTCCCTCCCCTCTGAGC
CCTATCCTGGGGTCAAGGGAGGTGATGGGACCCCTGGGAGAGGGGCGTCTATGTGCCCAA
TACCAGCCTGGCTCCCTCGGGTTCACCCCCATTACCCGGTACCCGGAGCTCCAGCTCC
AGCTCCAGCTCTGCCCCCTCTCTCCCTCATTGGGGTCAAGGTGCCCGTGGCCAGCACGTGC
GCGCAAGGCCATGTGGACAGCACCCACACACACTGCACCCACACCACACCTGTGCCC
GGGCCCACCTACCTCTTCCCCAAACCTTAGAGGCCTAGGAGCAGCAAAGCTTGGTTCT
CTACTCTCAGTTAAGTGCTCTCTGGGCTGAGAGCCTCCCCTCCTTCCCCTCCCCACAT
CCACTCAGAGCCCTCCCTGCACTGGCCCCCTTAGCCTCCTTTCCAAGGTGGCAGACTCCT
CTCGGCCCTCATCTGCCTGATGGCAATTCATCATCCAATCAAGGAGGGCTTCTTGGAGG
AAGGCTCTTTGATGTTTGTAGTCTGGGAGAGAAGGTGGAGGAGAAAAAGGAGTTGGGGT
GGCCTAGCAGGAGCTGAGTCACTTCCACAGGCAGCCATCAGCCAGCAGGACTGAGGCCA
GGGCTGCGTGGAGGGGGGAGGCTGTCTGTTCTGGGAGCTGGGACTGGGTACCGGGGAAG
GAGGGCTGCTGCAGGCTCTGGGTGCCTGGGGCTGGCTCCTGCAGGGCGGGCCTGTGAGA
GTGTTGGGGCCAGTGGAGGGGCTGGGAGCATTCAGGGGAACATTCCAGGGCGCCCTCTG

FIG. 20B

AGTAATGCTTGGCTCTGGGATTCCTCCTAGAGCCCCCTTAGGCACACCCGGCCAGGGAGC
 ACCAAGGCTCCGTCCGGAAGCGTCCCCCTCCCCCTTGAAGAGATGAGGAGGGGCCTTCTGGG
 CCAGGGTACCAAAACCTGCCACCAGGACAGAGTCCCCGAGGGAGCTCTGGGCAAGGTGG
 ACCTCGCAAGGCAACATCTGGCTGTTGTTTTTCTCAGATGATGGGGGGGGCACAAGTGTC
 CTCTCTTCGTACATCTCTCACCCCTAAAGGCATCTGCTGCCCATCTAAAAATCCCTAAGGC
 TGCCGCGCTCTTTCCTTCCCCCTCTGCACTGGCGGCCTTGGCCTCTTCCTTGTGATCGCCG
 AGCCCAAGCCTGCCCCCGACAAAGGTGAGGGGACTCCCGTGTCCCCAGCTGAGCTGTCC
 CTTTCCAGCCTTCTCTTTTCTCCTCCTTGATAGCTCCTCAGATCCAAGGATGCCACGG
 GCGTCCCTCCTTCTCCAGGCTGAGCCACGCGTGTGAAGGTGAAGTCTGCCCCAAAAGG
 CCTCCAGTGCCTCCCTGGGGATGTCTCTACCCCCCTCCCTCTGCTTTGTCCCATGCCCC
 TGTGTTCTCAGGTCCCCCTCACCTGTGCTCTGTCTTTACTCCAGGACATATCCCTGGG
 CAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAG
 GAGCCGGTCAGTGCCATGTCTCCCCGCCCTCCACAGGGGCCCTGAACCTCCAGCCCTTT
 TGTCTCTCCCTACATTACAGCTTCTAGTTTTGCTGGGGTCCCCAGAACCACCAAGTCACT
 ACTCCTATAGGCCCCCTGCCTCCCCCTGCCCCCTCAAGTGGGCAGAAGAAGGCACTGGGGTTT
 GGACATCTGGATCTCGTGAGCCCGCACACATGGAAGTCATTTAGCTTTCTCCACCCAC
 CTCCCTCTTTCCCTCCCTCCCTGGATGATCTGGGCCACCCCAACCCCAAGGAGAGAAAA
 TGGGTCCAGAGTTTGTGGGTCTGAAGCTTTTCAGGAGCCTCTAAAAAAGAAAAA
 AAAAAAGCACCAAAAAAGAAACCTTTTGCAAAGTTGACCAGAACATGTGACCCTGTGGACA
 CACTGCTGTCCCTCTCAGGGCCCTGCCACGAAGGCCTGAACCTTCAGCCTCACTGGCTCC
 TGTGGAATCCACTTCTGGTATGGGGGGGGCAGTGGTCACTCTCCTGATGTCCCCCAGATG
 TAAGACCACCCCATGTGCTTCTTCTGCAGGACGCTCTGCCCCAGCCTCTTCCCAATCCCG
 CTCTTCACACGCTTCCAGAATAACCATGCCCATCTGTTTGTGCCATAATATCTGTGCTG
 CAAACTAAGAGGGGCAGTAGCCTTGATATGCTCATTTTACAGAGGGGCAAACGGAAGCCCA
 GAGAGCTTGGGGAAATTGTCCATGGTCACACAGCTCTTTAGGCTGGGAGCCTGAGACCCA
 CTAAGGTCTGAACGATTTTAAACCATTTGGCTACACCCCTGCCCCCTCTAGAGAGCCCTCT
 TTGTTTGAATTTTTCAGCCCTACTGTCCAAATCCAGCAAGAGGGAAGGCAGGGGAGCATT
 GCCATGAAGGTGAGAGGCCCCCAGAGACCCAGCAGCTCCCAACCCAGGGCCCTCACTGG
 GATCCCCCTAGGCCATAAGGCCCCCCATTCCACTGGTCAAGCACGGCACTGGCCTGAGCTT
 TGAGATTGCCCTCCCCATCCCCAGGAGGGGAAGGCTGGACACACACTGGGGTCACTCTGC
 CTCTGGGCCTCCCTGTCTGTCTGGCCTGGGCTGTGACCAAGAGGAGAGCCCCAAAGGGGC
 TCTGCTTCCCCCACCAGGTGGGCCCTGCCCCCAGGAAGCCTGCCAAGATGGTACAGAAGA
 AAGAGTAGAGGCTAGGTATCCCCCTCCAAAGGCAGGAAACACTCACATTTCAAGATGAGG
 GGTATATATCAAGGGGCAGGGTACCAGGAGGGCAAGAGTAAAGATAGCAGGGGCTGCAGA
 GGAACAGGGACCTCGAGTATGGCCTTTTTCCCGGTGCAGACCTTTCCCCAATAAAGCAAG
 TGGCATTCCAGCCTCATGAGCTCATGCTGGAGGCCTTGTGGGGCCTGTGGCCAGGGAGGC
 AAGGACCATCTGCTCCCCACTTGCGAAGGAAGAACTCCCTCCAAAGACTCTGAGACCCTT
 GGACAGGGCCCCCAGGCCAGTGCATTTTGGAGAAAAGGAGTCGGGGGTAAACATTCCGA
 AGGCGCAGCAGCCTCCAGGAAGCTCCTGGGCCGGCTCCAACCTCTGGGCCCCAGCCAGG
 CTGAGTGGACAAGGGGGAAGTGGGGTGTTCACACAGGGTGGGAGACGCCAAGAGGGTGGG
 GGAAGGAGAGAGGGCTGGCCGTCCAAGCCAGCCTCCTGACACCTAGCTGAGAGCCAGTGT
 GCTCTCTTGGCTGGAATGGCGTCCATGTTTACTTCGTGGGTCCAGTGAAGCAGGTGTGCG
 AGCCGGAGGGACGGGGGCTGCTGGAGGCCCAGGAAAACCTTTGGAAGAGGGAGCAGTTTGC
 CAAAATTGGAAGTGGAGGAGTCAAATTTGAATTCTATAGGAAATGAGCAGCAGCTCATTT
 GGAACCAAGCCTCAGGTAGCAGAGGCTCTGAGGAGGCCCTGACCATGGCTACCCGATGCC
 CCCATAATGTCTCAGCACCCCTCTGTCTTCCCCTGCTTTTGTATGCCCTTCTGGGCATG
 AAAGAAGAGGGCGGGGCCAGGGGAGGGGCACCTTTCTGGGACCTCTGGTCTCTAGGGAGG
 ATGCTGGTGTGCTGGCAGGCTGTGCCAACGCCCTTCCAAGTGGCTGTTGTGAGGACTGC
 AAACATCCTGAGTTTGGGAACATCTTGTATGTTCTCACCTCCTCCACGCCCTCCATAGT
 ATGTGGGGGCTCTGCTGACTCCCCAGCCACGTTCTCCCCAAGAACTTCTCCCCAGCC
 GGCTCCACAGGCCACCTACTCCCTGGCAGGCAGGAGGCCTGGAGGCCACCATCTCAGCTC
 CACACTCTTTCTTGCCAGGTCTCGAAGCCAGACATGGGGCTGGTGCCCTGGAGGCTGA

FIG. 20C

AGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCAGTGAGTGCCAGGCTGGGGTAGGGC
TGGGAGGAGGGGATCAGTGTTGGGGGGCAGGGACTGACACAGATCTGTGCGGGTGGCTGG
ATGGGCAGAGGACCCAGAGAGGGTGCAGATGACAGGGAGAGTCACGCAGGCCTGTGGTT
GGCTCCCTGGAGGCTGAAGAGGACCGCTGAGGCTGTGAGCCCCGCTGTGGGGCACCTCCG
CCCTCCCAACCCAGGAGCGGCTTGTTAGCTCCCTGCTGGCGATGAGTGAGCACCACTA
GTGGACATTTGCAAGATATGCTGAGTCTAAAGAAATCCTAGAGGGAAAAGATGAGCCGGC
ACCCAGGCTAAGGGAATGGCAGGGACCAAGATGCGGTGGCTTTGGGAGGCCGAGGCGGG
CGGCTCACCTGAGGTGAGGAGTTTGAAGCCAGCCTTGCCAACATGGTGAAACCCCGTCTC
TACTAAAAATACAAAAAATTAGCCAGGCGTGGTGGCGGCGCCTGTAATCCCAGCTACTTA
GGGGGCTGAGACGGGAGAATCGCTTGAACCCCGAGGTTAGAGGTTGTGGTGAGCCAAGAT
CACACCACTGCACCACTCCGGCCTGGGCAAAGAGTGAGACTCCGTCTCAAAAAAGAGAA
AAAAAGAAAAAGAAAAAAGAAAAAGAAAAAGAAAAAGATGCAGTGGCTAC
ACTTGGGGGAGCAGGTTTGTCTGACCTGCCTGGAAGGTCTCCATCTACAGGGAGGGGAGC
AGGGGGGAATGAATTTGGAGAGTCCCAGGAGGGCCAGATCACAGAAGGCCATTTTGGTGC
TCAGTGTCTGGACCATCCAGAGCCAAAGATTTTGAAGTGGGGAAGGGACAGGCAGACCT
GTGCTCAGGAAGGTGCCTTGGGCTGGGTGGGGTGGGTGTCCGGGCTGGAGCGCAGGCTCT
TAAAACCACCCAGATTATGTTATCAGTATATATCACCTACTGAGTGCTTGACCGCAGGCG
CTGTTCTGAGCACTTGACACGTATTTTATTCTCCCTCGTGGAGTCGGATGGACAGGGAAC
AAACTCTAGTTCCTGCTGCCCCAACCATATTTTCCCGACGTCCCTACCCTTTCAATGGGG
TGGTCACATCACCTACCTCCTAGGGTGGCGGGTGTGTGTGGGGCAGGGGTAGGGGGCAGA
GCTGGGGCAGGTGGTGGAATGCCTGGGAGGGGGGAAGCAGCCATCATTAGCGGGTGGTCT
GGAGGTAATGAGGCCAAGGTGAGGTGGGTAAAGGATTTTCTTTAAAGAAGACAGATTGA
CTTATGATTGATCCATCCGTGTGGGAAAGATCCTGTTGAGATGGAGCCTGAAGATGGAAT
CATTACCGGAGTGGGTGTGGAGAAGGCAGGGAGGGTGGGAAGCAGCGTGGGCAGGTGGCGA
TTCTGTTTTCTCTGGAGGCAGGGGGTGGAGCATCAATCACTGAAGGACAGGTGGGAGGTAT
GTGGGGTCTAGAAGTCTGAGGAAAATATTTCAAGGATCTAGGGCAGGTGGGGGCAAGAGG
GTCGACCAGATGCCCAACAAAGGAGGGCAGCAGGCAGGGGAAGTGGGGGAGGTCAACGCA
TTTCCCCAACTCCAAGTCCCATTTCTTCGGCAGTGTCTCCTGACTCCTCCCCCTCCCGATCC
TGTGGATCCTGCTGCCTGCTGCAGGTCCCCTGGGAACCAAACTCTTCCCCCTATTCCCA
CTCCTCCCCGGCGTCTCCTCCCTGGTGCTTCCCATATTCACATCTCCCACAACCTAAGCCATC
ACCAAGGCTCCTTCTCTAGCCCCAAGAGTTTCTGATCTGAGCAAGTCACCATTGCTCCT
GTCCCTTCCCTAAGACACACTGTGAGTGTCTCACTCATAAAGCTGCTCCATTAGCATTGA
GGGAGGAAGGCTGGGAGACATCCTGGAGGAGGCAGGGAAGCTGAATTCAGTGTTCCTT
GTAACACCCCTCTCAGCAGGCTGTGGCCCCCAGGATACATAGAAACCCACTACGGCCCCA
GATGGGCAGCCAGTGGTGCTGGCCCCCAACCACACGGTGAGATGCTTCCATGGGCTCTGG
GATGCACCGCCAGAGGTACCCCCCACCATTCTACCCCTACTCCTCCTTGCAATTCCTAA
GGGGCGGTTGGAGCCAGCCCCCTACCACACCCTCCCTCTTGCCCCCTCTTGCTCCAGCCCTG
GCTGAGATTTGGGGCTGGCCCCCTTCTCCCTAGGATCATTGCCACTACCAAGGGCGAGTA
AGGGGCTTCCCCGACTCCTGGGTAGTCTCTGACCTGCTCTGGGATGAGGTGAGCTCTG
GGAGAGGAGGCTGGGCCTGGGATGGGGAAAGAGCTCCCTCACACCCGCTCCTACCCCTCT
GCACCCTAGTGCCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCC
ACCCCGGGGCTCCAAGGACTTCTCAACCCACGAGATCTTTCGGATGGAGCAGCTGCTCAC
CTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCCTTC
TGGTGGTCCCCAGAGCAGGGTCAGGGGCATCGATCGGATGGGAGTGGGAATGCTGTATCT
ATAGCCCTCCAAATCAGAAGAGACAGGAATTCACAGGCCTCGAGTCCCAGTATTTTTATT
GAAGTCTGAAGAAACAAGTTCCAGAAAACATGTTAAACTTCTTCTGGGAGCTGGGGTTG
GGGGTCAGGGCTCAAGCCCAGCAGCTTCCACTCAGGGTCCCCATTTGCACCTCCGCAGGG
CAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACAC
CCTGGTGAGGAGAGACCCAGGGGTTGGCGGGGTGAGGATGGGGCCAGCTCAGCCCCCTC
AAGCCACCGGATTTCTGCCTTCCCAGTTCTTGACTCGGCACCGAACTTGAACCACACC
AAACAGCGTCTCCTGGAAGTCGCCAACTACCTGGACCAGGTGGGGGCGGCGGGGAGAGA

FIG. 20D

GCGGTGATGGGGGTGGCGGCGGCAGGACAGGCAGGTGCTGGTGGGGTTTGGGGAAGAGGA
 AGGGCGCCCCACGAAGGACCACCGGCGCGATGGGGCGCCCTGTCCCGGCTTCAGCCCCGC
 CTCGCCCTCAGCTTCTCAGGACTCTGGACATTAGGTGGCGCTGACCGGCCTGGAGGTGT
 GGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGGGCCTTCC
 TGCAGTGGCGCCCGGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGCTCACGT
 GGGTGCCTCTGACCCGGACGCGGGTCCCAGGTGGGGCGGCCTCACCTCCCGGCCCGCCT
 GGTACGCGCGCTCCGCCCCAGGGGCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGC
 GCCCCGTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGAGCACGGTGAGCCCCGC
 GGGCGGGGGCGAGGGAGAGACAGGAGGCTCTACGGCCGCGAGTACCGCCCTCCCACGGCC
 CCCCAGGACCACTCGGAGCTCCCCATCGGCGCCGAGCCACCATGGCCCATGAGATCGGC
 CACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGCTGCGTGAGGCTGCGGCCGAGTCC
 GGAGGCTGCGTATGGCTGCGGCCACCGGTACGCGGTGGGGGTGGGGGTGCGGCCGAGTCC
 GGCGGCTAGTCTGGGGACTTCCTCCGCTGCGTTTCTTTGGTCCCTCAGTTTCTCTCT
 TCTGTAAAATGGGGATAATGATCATAGTGTCCGCTTCAGGGTGGTTTATGAGGCTTAAAG
 GGAAGAAGCTCAGGCAAAGTGGATTCTCAACGGTATGAAGATTATTTTCCGAGTAACCTG
 GCGAGGTTACTCCTACACCGGGAGGAGACCGTCCGGTTCGCGATTCCACCTGGGTCCCG
 GGCTGCTCACTATTGGGGCCGCATCGTCCCCTGTCCCGCTTGTGTGTGACTTTGCGCGG
 GTTACTTCCCCTCTCTGGGCTCTGCGCGTCTGGCGGCTGTAGCCAAGCCAGGGGTGGGG
 ATCAGAGAAGCGCGGGGGTTGGGGGACTGTCCCTCCATGCCCAATGCCCTCCCCGTGCCG
 GTAGGCACCCGTTTCCGCGCGTGTTCAGCGCCTGCAGCCGCCGCCAGCTGCGCGCCTTCT
 TCCGCAAGGGGGGCGGCGCTTGCCCTCTCCAATGCCCGGACCCCGGACTCCCGGTGCCGC
 CGGCGCTCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCC
 AGGTTAAGTCGGCTCGCCCGCCCCACTTGCCCTCTCCGCTCAGGTCTGGGGCGCTGCG
 CCCTCACCTGGGCCCTTCTTGCCCTTCTGGTCCCAGGAGTGCCGCGACCTCTGCTGCTTT
 GCTCACAACCTGCTCGCTGCGCCCCGGGGGCCAGTGCGCCACGGGGACTGCTGCGTGCGC
 TGCCCTGGTGAGGGCATGGAAGGTTAGGGTGAGGGTTTTCGGGGAGCTTGGGAGCCGGCCT
 GTTGGCCTTAGTTAATTGGTGCCCTCAGGTTCCCCCGTTGGGTGCTGGGCTTGGGTAGGC
 CTGGCTCCCCAGCTCCGAGCCGCGCTCTCGGCATGGACCTCTCACTGCACGTGGCCTCT
 CTCTGCCTTCCCCACCACCCGTACCTGCGCAGCTGAAGCCGGCTGGAGCGCTGTGCCGC
 CAGGCCATGGGTGACTGTGACCTCCCTGAGTTTTTGACGGGCACCTCCTCCCACTGTCCC
 CCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGCGAGTGGCTACTGCTGGGAT
 GGCGCATGTCCACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTGGTGAGAGGACA
 CGAGACCCCTTGACCCCTGCCCCCATCCTCTGGTGGGGCCAGTTTTCTACTGTGGGGAA
 GATGGGCAGGGAAACTGAGGCCCGCTGAGCGCAGCCCCCTCTCCGAGCTGCCCCAGCCT
 GGCCCATGCTTCTCAGGCTCCACCCAGCTCCCGAGGCTGTTTCCAGGTGGTGAACTC
 TGCGGGAGATGCTCATGGAAACTGCGGCCAGGACAGCGAGGGCCACTTCTGCCCCTGTGC
 AGGGAGGTAGGGAGTGGAGCTGAGTGGAGGGAGCAGAAGCTATGGAGTGGGTTTGGGGAA
 GGGGGGTACTGCAGCTGTTGACCCCCCTCTACTTCTCCCGAGGATGCCCTGTGTGGGA
 AGCTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACT
 CTACCGTTACCTAGATGGCCAGGAAGTGACTTGTGGGGAGCCTTGGCACTCCCCAGTG
 CCCAGCTGGACCTGCTTGGCCTGGGCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAA
 TGGTGAGCTCTGCCCACCCGACCCCTCCTTGCCGTTTGAATCCCGCAGGCCAGTGTCCCC
 CTCCTGCTGGTGCACTGCCCCGTAGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCT
 TCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTGAGAGCCCAGGAG
 TGGGGGTGACCTTGGGGTTCTTAATCCTACGTGACCCCTCCTCTTCTCTCTGAGGTT
 TGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAG
 CCAGGCTTTGGTGCCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAGTATGCCAGTGGGG
 GGCATGTGGGCAGGAGCTGGGGTGGTGACCTGCTCAGGACTCAGCGCCCTTCCCCCAA
 TCCCCGAGACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTCTGC
 TCCAGGGGCGGCGCTGGCCTGGTGTGTGCTACCGACTCCAGGAGCCCATCTGCAGCGAT
 GCAGCTGGGGCTGCAGAAGGGACCTGCGTGCACTGGGTAGGCTCCGAGCGCCTGCTTCC

FIG. 20E

TGAGCCTACTCCTGCGGTTCCTCCTCAGAGCTCTGCTGGGGCTGTGGGAGCTGGGGCA
GGCCCTCAGCCTTGCCCCCAGGTGCAGAGAGCAGCCCCAGAGGCCATGGAAAGAAGTAGC
TTTGAACAGGAGGTTCAGTGGCCTCCAGTCAAGCGAGGGGGTGGATCCCTGCCCCACC
ACCAGCACGCAAGGCATGGCCCTCTACCTCCAGTACAGCTCCTCTTGTCCACTCTCCT
GCTTCTCCCACCAGCTGGCTGCCTCACCCTTGACTTCGCCCTGTTTTTCCCTGGCTCAGA
TTGCAGTCCCTGTACCATGCTGCCCCCGGAGGCCTGTCCAGCCTCTGTCTCACCAGTTTT
CGGCCCTTTGCCACTTCCTCTGCACAAATCACCTCTGTCACCCCCTTGAAGTTCCCAAAT
GCTGGGCCCAGCACATCTTTTCACTCCATAACCACTGGTCAGCTGCGGTGCTGGCTGCCCC
TGTGCCAGGGCCCTGCCTTAACCCAGTTCTCTGTGACCTGGGTGGTGGCGGAGTGGGGAG
TCACATAATACTAAGCATGGCTGTCTAGGACTCACCTGCACCAGGGCCCTAGGCAGGG
CAGGCACTCTGTGGCCATGTCTGACATAGCCTGGTCTTGGGAGTGTCTCCGGGCAAGCCAA
GGGAGATGGCATGATTTGGGCCAGAGATGGGGGCAGAGGGCATAACAGACAGGGGCAGGG
CACCACCTGGGCCCCGGGTGGCAGCTAAGAGGACCCTGACAAAGCGAGTTGTGATTGAGG
GTCTGTGGGCAGAGGAGCAAGGTGGCCAGAGCCTGGCGTGTGAGCAGCAGGGGGCGCTG
CAGAGGGTGGCGGTGCTTCTCATCCCCAGGCGGGAGTCTCAGGGCAGGGGAGATGTTT
TGAAGGAACATCACAGGAAATGACAAGGCCTTGGGGGATGGGATGGGGACAGTCAAAGAT
GGCTTGAATCATCAAGGGCAGCAGGGCACCCAGGGGCAAGGAGAGCAGACATAGCTGCC
GAAGGGGCGGACATCCAAGGTTCTTTGGAAGCTGAGCGATGCCAGCATCTGGAGAGTGCC
AGGCTGCTGGGTGGTGTGAGAGCCTGGAGGAAATGTTAGGACTAGAGAGAGGAGGTGCCA
GCCGAGGGCATGAGGCTCACTTGGAGCCTGGATCCCAAGGCTCCCCTGAAGAGGGAGCAG
GAAGGGAGCTGAGAGGGTGACTTGGAGCAGATGGGTGCCCAAGAACTCAGTAAACGCA
GAATCCCTGGGCTGGACACCATGCTGCGGGGAGGCAATAACCCACTCAGGATCACTGTG
CCAACCTCCTGGACTCTTATCAGTTGCTCAGCCCCAAAGATGGCCCCACACAGGGACCAC
CCCCCTGGGCGGCGTTCACCCCATGGAGTTGGGGCCCCACAGCCACTGGACAGCCCTGGCCC
CTGGGTGAGTGAGGCACCAGGGGGAGGTGGAGAGGGAAGGGAGAAGGGGCTCATGC
CTCCTGCCTCCTTCCAGATGGGCAGCACCCAGTCACCTTGAGTCCCCTATGCCCTCCCC
AGCCCCAGGGTCTCCTGCTGACCATATTCAACAATTTACCCTCCACCATTCTCCCAGA
CCCTGAGAATCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCC
TGACCCCCAAGGTAGGCAGGGACCTGGATTCAAAGCCTCCCCCTCTCATCGCCCCACCCTC
CCACCTCTCCCACCCCTCAGTTTGCTGCCCCCTAATCAGGTTTCTGGGCTCAGGTTATTA
TGGAATGAGTTTATGACCTCTTGGTTATCATGGAGACCAGGATGCTGGAAGCCCCTGGG
CTGGGGAGGGAGAAGCTGTGGCTTTTCTGGATCACTGGTCTCACTGAGTGAGGATGGG
CTCTCTGCCACACAGCTTGAGCCTGGGGCCCGAGTCTTAGGGGACAACATATCCTCCT
CATTCTCAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTA
AAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTGAACTGCAG
GGGCAGAGCCAGTGAATCACCGGACCTCCAGCCTGCAGGCAGCTTGAAGTTTCTTCC
CCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACACTAGAAGTTCTGAG
GGCTGGAGAACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAA
AGGTCACACAGCCCCTGACCTCCCTCACAGTGGAGGCTGGGTAGTGCTGGCCATCCCAA
AAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCCTACATGCAATTTCCACGGACCCAGCTC
TGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTCTGACTGA
GTCCCACTCCCCTGGAGCCTGGCTGGCCTCTGCAACAAACATAATTTTGGGGACCTTC
CTTCTGTCTTCTTCCCACCCTGTCTTCTCCCCTAGGTGGTTCTGAGCCCCCACCCTCAA
TCCCAGTGCTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTCCCCCATCTGT
GTGTGTGCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGA
AAGCATGTTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCT
GGGTAGGAGGATCACCAGAGGCCAGGAGGTCCACACCAGCCTGGGCAACACAGCAAGAC
ACCGCATCTACAGAAAAATTTTAAATAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCT
AGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAG
CTATGGTGGCACCCTGCCTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATA
AATTTTAAAAAGACATATTACACTTGGACCTTGGTTAGTCTTTTCTGTATGTAAATTCAA

FIG. 20F

CCCATGGGGTGCCCTGAGGACCACACGGGGTGGTGGTTGGCGGGGTGGTGGTTGGTGGGG
TGGTGGCTGACGGGGTGGTGGCTGGCAGGCCGAGCCTAGATGGCAGCCAGAGCCCCAGGC
ATGTGTCTGGGCACAGGACGGTGTGCTTAGTTTGAACACCCTCTTTGCTCTGTCACTCC
TGCCTCCCTTGGGCGTTTACATTCTCCCATTTGCTTCATGCAAGAGCTGCTGAGTGGCCTA
TATCAGCCAGCTGTTGCCGCATAACAAAACCATCCCAAACTGAGTGCAGGGAGGCAACT
TCACCTCGGGCTCCACTCCACAAGCCCAAGGGGCCAGGTGAGAGTGCTCTCTAAAGCCCC
CTCCTGCCTCAGTTGTAGTTGCAAAATTTTAATTTATGAAGGTGACTGATGACACAGAGG
CCAATGCTGTTGAAATAAGTTATTACTCACAGTTTCCACCATGCAGGGCCACAGTGGGG
AGGCACTAGGTTTGGTCCAGGGACAGAATCAGGAGCGAGTGGAAGGCACAGGCCACAGCC
CACAGTGCCGTTTCCACTGGGGAGGCAAGGCAGGCCAGGGGAAGAGGGTAGGATTGGCAT
TTTGAATCATTCTGGTGGGGTTTGGGGCGTGGGGTTGGGCTCTAATTGTCTGGGTAGGTG
CCTGGCCCTGAGCTGGTTTAGGGCAGGGGAAATACTGGTTTCGTATGTGAGAGTTCCTTG
AAGGGGGTGGTTGGTGTATGGACTCAAGACTGGTCGGTTTGCATATGAAAGGCATGAGTT
GTTTCTGATCTCCAGGAATCAAGCAGTTTCTCTCCAGCCAACAAGCCCCACCCCGAGAT
GTTAAACCATCATAAAATAGAGAATCTAAGGCCAGGCATGGTGGCTCACGCCTGTAATCC
CAGCACTTTGGGAGGCCAAGGCGGGAGGATCATTGAGGTGAGAAGTTCGAGACCAGCCT
GGCCAATGTGGTGAAACCCCATCTCTACTAAAAATACAAAATTAGCCCGGTGTGGTGGC
ACGTGCCTATAATCCCAGCTACTCGGGAGGCTGCGGCAGGAGAATTGTTTGAACATGGGA
GGTGGAGGTTGCAGTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGGGCAACAAGAGCA
AGACTCCGTCTCAAAAAAAAAAAAAAAAAAAGAGAGACTCTAAAAATACACGTTAATAT
ACCTCCCCCGCTCTTACCCTTCAGGAGGGGGTGTCTAGACCCCGCGGGACTCCAGCTACA
AGGGACCCCTGGGGAGGCCAACTCTGCCCTCTTGGCTAATCCCCAAGACTGCCCAGCACCC
CCTCCACCCCTTCTCCATTCAGTGGCGAACCTGGGGAGGCCACGTGGGAAGGAAAGAGG
GCTCTAAGAGGGGAGGCCCCAGACTGGGGGAGAGGCCTGTCTGGAGCCCAGGATCACCTG
GCTGTGCTGCAGAACTGGAGAAGAGAAGCTCAGCAGAAAGGAGCTGGCATGGGGCCAACA
GCAGAAAAGCAGGAGGCACGCAGAAGTGACTGGGAAGCAGGAGGGTAGGCATGGACCCTG
AGGCTGAGCAGGAGGTACTGAGGGGCAGAGTGGACGCTGAGCTGGGGGTAGCGAGCGAGC
CCAGCTCAGCTGTGACGCCCTCTGTTTGGCCACCCAACTACCAGCTACTTGGGCTGCCCC
GGGAGGAACTGGGCTTCCTCTGACATTCTGTGGCCTGCGGCCATCTGTACACCTTCTTC
TCTCTCTGCCCCCTCCCTTGACTTGTGGCACCCACAGACAGGTGGGAGAGTGTACCTGCCC
TGTGTGGTCAGAGCTTGGTTTTGAGTTTCCCTTCCCTCACCCCTCTTTCCTCCACACGCC
AAAACACAAGAGGATGTGTGAGAGGCCTGTGAACCAGAGCAACTCCATCCTGAATAGGGG
CTGAGCAAAATAAGGCTGAGACCTACTGGGCTGCGTTTCCAGACAGTTACAGCATTCTGC
GTCACAGGATGAGATAGGAGATACAGGTGATAAAGACCTTGCTGATAAAATAGTTTGCAG
TAGGCCAGGCGCGGTAGCTCACGCCTGTAATCCCAGCACT

FIG. 20G